

101st Annual Meeting of the American Society of Parasitologists

MEETING PROGRAM



**ASP thanks the following individuals
& organizations for their
generous support:**

FGCU

Scholarly Innovation
& Student Research

THE UNIVERSITY
OF **TAMPA**
COLLEGE OF NATURAL
AND HEALTH SCIENCES

UF | Emerging Pathogens Institute
UNIVERSITY *of* FLORIDA



Visit
Orlando



CLYDE BUTCHER | ARTWORKS

Thanks to Everyone Who Helped Make this Meeting Possible ...

The American Society of Parasitologists gratefully acknowledges all those whose support, sponsorship, time, and efforts made this year's annual meeting possible.

Special thanks to the ASP Local Organizing Committee

Christina Anaya, Florida Gulf Coast University (canaya@fgcu.edu)

Chris Blonar, Nova Southeastern University (cblanar@nova.edu)

Emily Durkin, University of Tampa (edurkin@ut.edu)

Gabriel Langford, Florida Southern College (glangford@flsouthern.edu)

Kaitlin Gallagher, Florida Southern College

American Society of Parasitologist's Discrimination Policy

Statement of Policy: In accordance with the bylaws of the American Society of Parasitologists (ASP), the Society will afford an environment free from discrimination, harassment, and retaliation. The ASP will not tolerate actions, statements, or contacts that discourage the free expression and exchange of scientific ideas. This includes unequal treatment or harassment of any person based on their age, gender, gender identity or expression, marital status, sexual orientation, race, color, national or ethnic origin, religious identifications, beliefs or practices, disabilities, veteran status, or any other reasons or expressions that are unrelated to their scientific merit. Harassment, sexual or otherwise, shall be considered as a form of misconduct and violators will be subject to disciplinary actions, including expulsion from a society function or from the society itself.

Definition of Sexual Harassment: Sexual harassment refers to unwelcome sexual advances, requests for sexual favors, and other verbal or physical conduct of a sexual nature. Sexual harassment does not refer to occasional compliments of a socially acceptable nature. It refers to behavior that is not welcome, is personally offensive, debilitates morale, and therefore, interferes with a collegial atmosphere. The following are examples of behavior that, when unwelcome, may constitute sexual harassment: sexual flirtations, advances, or propositions; verbal comments or physical actions of a sexual nature; sexually degrading words used to describe an individual; a display of sexually suggestive objects or pictures; sexually explicit jokes; unnecessary touching. What is perceived as acceptable to one person may be unwelcome by another. Those who have positions of authority or higher rank should be aware that others may be reluctant to outwardly express objections or discomfort regarding unwelcome behavior or language.

Other Types of Harassment: Remarks and behaviors based on other protected characteristics are also unacceptable to the Society. These include stereotyping, slurs, derogatory jokes or statements, and any hostile or intimidating acts.

Policy Scope: This policy applies to all attendees and participants at ASP meetings and functions, including social functions, tours, or off-site activities during the course of meetings and functions, and includes all members, guests, staff, contractors, and exhibitors.

Reporting an Incident: If any individual covered by this policy believes that they have experienced or witnessed harassment or bullying they should contact the Society's designated individual. No complainant will be required to discuss any incident with a respondent; no respondent will be required to discuss any incident with a complainant. All individuals (complainant or respondent) may bring an accompanying individual of their choice with them for support at any point when they discuss the matter with the Society's designated individual, or during any course of an ensuing investigation.

Because allegations of discrimination, harassment and misconduct are sensitive matters with the potential to negatively impact the reputation of individuals, institutions, and/or our Society, confidentiality and discretion throughout the process is expected from all parties involved and is assured from the ASP's designated individual and all involved in the investigation.

Regardless, a complainant may speak in confidence with the Society's designated individual without involving an official report, an investigation or a respondent. All complaints that are received will be treated seriously, and will be addressed promptly if that is the wish of a complainant. Any incidents of sexual assault should be immediately reported to the police. Note that many local and regional governments also consider a variety of behaviors to be reportable crimes regardless of the wishes of the complainant, respondent or of the Society.

Investigation: Following the official report of an incident, the Society's designated individual, in consultation with ASP Council, will name an impartial investigator; usually an elected officer or Council member, and the respondent will be promptly notified. No one who has a conflict of interest with respect to the complainant or respondent will serve in this role. A complainant will be asked to file a formal written complaint; the respondent will be notified immediately and prior to any discovery procedures. A respondent will be invited to respond to the complaint and allowed to bring evidence. The Council of ASP reserves the right to interview other individuals as witnesses at its own discretion. The investigator is allowed to seek counsel if they are in doubt as to how to proceed.

When the investigation is complete, the findings will be communicated to the elected officers, as well as both to the complainant and respondent. Those officers without a conflict of interest will decide on appropriate disciplinary actions.

Retaliation: The Society will not tolerate any form of retaliation against individuals who report an incident, against those who are subject to a complaint, nor against those who participate in an investigation. Retaliation will be considered a form of discrimination in and of itself and offenders will be subject to disciplinary action, up to and including ejection from the Society.

Disciplinary Action: If an individual harasses, retaliates, or knowingly makes a false claim, they will be subject to disciplinary action. These actions might range from a verbal warning to a request to leave the meeting or function without refund of fees and a reporting of the incident to the person's employer. Should repeated complaints, patterns of inappropriate behavior, or other events emerge, the Society's by-laws permit its Council to exclude and eject members through a process that has no appeal.

Appeal & Questions: Should any person be dissatisfied with the result of an investigation or disciplinary action, they may appeal to the President of the Society, or to the highest-ranking officer without a conflict of interest. Questions concerning the policy can be directed to an ASP officer or the ASP designated individual.



Meeting Program

Welcome!!

We would like to welcome you to the 101st Annual Meeting of the American Society of Parasitologists (ASP).

The ASP is a diverse group of approximately 500 scientists from industry, government, and academia who are interested in the study and teaching of parasitology. Founded in 1924, ASP members have contributed not only to the development of parasitology as a discipline, but also to primary research in systematics, medicine, molecular biology, immunology, physiology, ecology, biochemistry, behavior, and more.

Scientific Program Officers

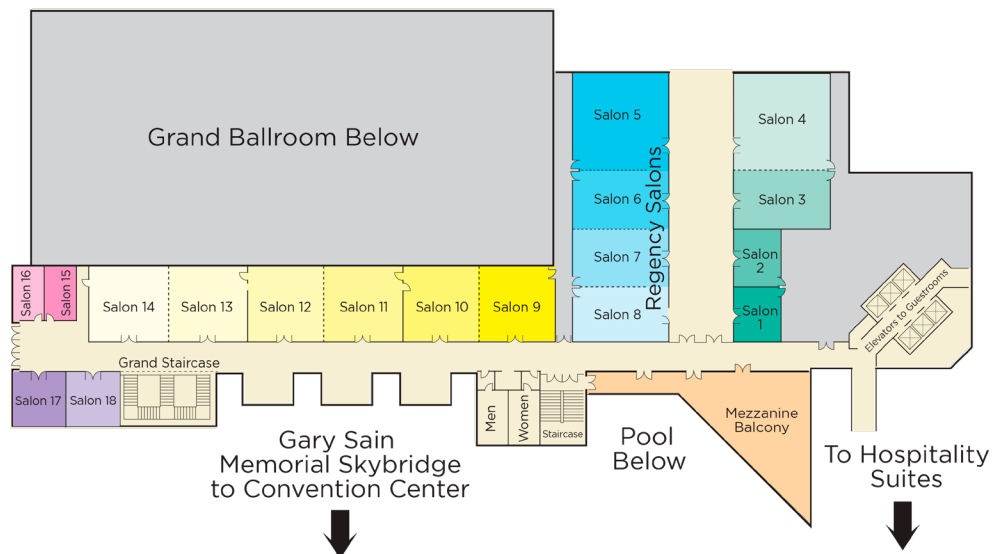
Susan Perkins & Kirsten Jensen (amsocparasit.meetings@gmail.com)

Map of Meeting Rooms

LEVEL 1 - GROUND FLOOR



LEVEL 2



General Schedule

Day/Times	Activity/Function	Room/Space
Sunday, 26 July		
7:30 am–5:00 pm	Registration	Ballroom Foyer, Desk C
8:00 am–Noon	Council Meeting	Salon 14
1:00–2:30 pm	Session IA: Taxonomy & Systematics 1	Salon 9/10
1:00–2:30 pm	Session IB: Ecology 1	Salon 11/12
2:30–3:00 pm	Coffee Break	Alcoves Level 2
3:00–4:00 pm	Session IIA: Taxonomy & Systematics 2	Salon 9/10
3:00–4:00 pm	Session IIB: Chemotherapy	Salon 11/12
4:00–5:00 pm	President's Symposium	Ballroom D
5:00–6:00 pm	President's Address	Ballroom D
6:30–9:00 pm	Welcome Reception	Ballroom C/Foyer
Monday, 27 July		
7:30 am–5:00 pm	Registration	Ballroom Foyer, Desk C
8:30–10:00 am	Session IIIA: Ecology 2	Salon 9/10
8:30–10:00 am	Session IIIB: Host-Parasite Interactions 1	Salon 11/12
10:00–10:30 am	Coffee Break	Alcoves Level 2
10:30–Noon	Session IVA: Taxonomy & Systematics 3	Salon 9/10
10:30–Noon	Session IVB: Host-Parasite Interactions 2	Salon 11/12
Noon–1:00 pm	Student Lunch Vortex	Salon 13
1:15–2:45 pm	Session VA: Ecology 3	Salon 9/10
1:15–2:45 pm	Session VB: Host-Parasite Interactions 3	Salon 11/12
2:45–3:15 pm	Coffee Break	Alcoves Level 2
3:30–4:30 pm	Eminent Parasitologist Lecture	Ballroom C
4:30–5:30 pm	Business Meeting (open to all; student attendance encouraged)	Ballroom C
Tuesday, 28 July		
7:30–11:00 am	Registration	Ballroom Foyer, Desk C
8:30–10:00 am	Session VIA: Evolution	Salon 9/10
8:30–10:00 am	Session VIB: Ecology 4	Salon 11/12
10:00–10:30 am	Coffee Break	Alcoves Level 2
10:30–Noon	Session VIIA: Genomics	Salon 9/10
10:30–Noon	Session VIIB: Ecology 5	Salon 11/12
Noon–1:00 pm	<i>Journal of Parasitology</i> Editorial Luncheon (by invitation only)	Salon 13
1:00–2:00 pm	Students' Symposium	Salon 9/10
2:00–4:00 pm	Poster Session & Palettes & Parasites	Ballroom D
2:15–2:45 pm	Coffee Break	Ballroom D
4:00–5:00 pm	Student Business Meeting (for students only)	Salon 9/10
6:00–9:00 pm	Auction Preview & Auction	Ballroom C

Wednesday, 29 July

8:45–9:30 am	Session VIII A: Collections	Salon 9/10
8:45–9:30 am	Session VIII B: Host-Parasite Interactions 4	Salon 11/12
9:30–10:00 am	Coffee Break	Alcoves Level 2
10:00–11:00 am	H. B. Ward Medal Lecture	Ballroom C
11:00 am–12:30 pm	Award Presentations* & Adjournment	Ballroom C

*Awards being presented include the Clark P. Read Mentor Award, the Ashton Cuckler New Investigator Award, the Best Student Presentation Awards, and the Marc Dresden Student Travel Grant Awards.

Schedule Overview

	Sunday, 26 July	Monday, 27 July	Tuesday, 28 July	Wednesday, 29 July
7:00 am				
8:00 am				
9:00 am		Session IIIA: Ecology 2 (Salon 9/10)	Session VIA: Evolution (Salon 9/10)	Session VIII A: Collections (Salon 9/10)
10:00 am	Council Meeting (Salon 14)	Session IIIB: Host-Parasite Interactions 1 (Salon 11/12)	Session VIB: Ecology 4 (Salon 11/12)	Session VIII B: H.-P. Interact. 4 (Winston 1C)
11:00 am		COFFEE BREAK	COFFEE BREAK	COFFEE BREAK
Noon		Session IVA: Taxonomy & Systematics 3 (Salon 9/10)	Session VIIA: Genomics (Salon 9/10)	H. B. Ward Medal Lecture (Ballroom C)
1:00 pm		Session IVB: Host-Parasite Interactions 2 (Salon 11/12)	Session VIIB: Ecology 5 (Salon 11/12)	Awards Presentations & Adjournment (Ballroom C)
2:00 pm	Session IA: Taxonomy & Systematics 1 (Salon 9/10)	Student Lunch Vortex (Salon 13)	JP Ed. Luncheon (Salon 13)	
3:00 pm	Session IB: Ecology 1 (Salon 11/12)	Session VA: Ecology 3 (Salon 9/10)	Students' Symposium (Salon 9/10)	
4:00 pm	COFFEE BREAK	Session VB: Host-Parasite Interactions 3 (Salon 11/12)	COFFEE BREAK	
5:00 pm	Session IIA: Tax. & Syst. 2 (Salon 9/10)	COFFEE BREAK	Poster Session & Palettes & Parasites (Ballroom D)	
6:00 pm	Session IIB: Chemotherapy (Salon 11/12)	Eminent Parasit. Lecture (Ballroom C)	Student Business Mtg. (Salon 9/10)	
7:00 pm	President's Symposium (Ballroom D)	Business Mtg. (Ballroom C)		
8:00 pm	President's Address (Ballroom D)			
9:00 pm				

NOTE TO PRESENTERS

Please upload your presentation as early as possible—preferably the day before your session. If presenting in the morning, upload by 8:15 am; for afternoon talks, upload by 12:45 pm at the latest.

Detailed Schedule

Sunday, 26 July 2026

● student presentation in the Best Student Presentation Competition

7:30 am–5:00 pm

Registration

Ballroom Foyer, Desk C

8:00 am–Noon

Council Meeting

Salon 14

1:00–2:30 pm

Sessions IA & IB

Session IA: Taxonomy & Systematics 1 Salon 9/10		Session IB: Ecology 1 Salon 11/12	
Presiding: Florian Reyda (State University of New York at Oneonta) Delaney Long (State University of New York at Oneonta)		Presiding: Valerie McKenzie (University of Colorado, Boulder) Dana Calhoun (University of Colorado, Boulder)	
1:00 pm	● (1) <u>Abigail Finch</u>, Jillian Detwiler Temporal analysis of genetic diversity in a multi-host nematode parasite (<i>Parelaphostrongylus andersoni</i>) undergoing secondary contact		● (7) <u>Maggie Young</u>, Makala Fabrizio, Marion Baker, Jim Page, Brandon Baker, Caroline Cooper, Amory Cook, ... Tyler Achatz Detection of <i>Anguillicoloides crassus</i> (Nematoda) and a survey of endohelminths of American eels in Georgia, USA
1:15 pm	● (2) <u>Alexandria Nelson</u>, Wesley Neely, Cory McKinstry, Kenzie Pereira, Jeff Beane, David Rodriguez, Skylar Hopkins A new genus and species of trematode parasite (Plagiorchioidea: Ochetsomatidae) from the oral cavities of snakes		● (8) <u>Katherine Buschang</u>, Robert Poulin, Clément Lagrue, Jerusha Bennett A bird's-eye view of <i>Toxoplasma gondii</i> in New Zealand: Prevalence across hosts, habitats, and ecological traits
1:30 pm	● (3) <u>Douglas Stephan</u>, Gregory Deets, James Bernot The copepod genus <i>Eudactylina</i>: working towards a stronger grasp of elasmobranch gill parasite systematics		● (9) <u>Jasmine Groves</u>, Jasmine Childress Parasites on the urban edge: A review of host–parasite shifts in cityscapes
1:45 pm	● (4) <u>Katherine Hanselman</u>, Kirsten Jensen Fretting over guitarfishes: Exploring patterns of diversity of species of <i>Polypocephalus</i> (Cestoda: Lecanicephalidea) parasitizing members of the Rhinopristiformes		● (10) <u>Connor Goldy</u>, Anil Baniya, Perla Achi, Cullen McCarthy, Adler Dillman, Lanie Bavier, Robert Pena, ... Riley Rackliffe Surveillance of <i>Heterobilharzia americana</i> in recreational water bodies of the Colorado River basin: Implications for canine health
2:00 pm	● (5) <u>Netanya Williams</u>, James Bernot Discovery of 10 new species expands our concept of morphological diversity in the parasitic copepod genus <i>Pseudotaeniocanthus</i>		● (11) <u>Santiago Escobar-Alfonso</u>, John Brule, Stephen Bullard Molecular detection of White Spot Syndrome Virus (WSSV) and Yellow Head Virus (YHV) in wild-caught northern brown shrimp (<i>Farfantepenaeus aztecus</i>), northern white shrimp (<i>Litopenaeus setiferus</i>), and rough mantis shrimp (<i>Squilla empusa</i>) from the Gulf of America
2:15 pm	(6) Scott Gardner, <u>Altangerel Dursahinhan</u> Helminth parasites of Galápagos mammals: A new cestode of the genus <i>Raillietina</i> from the endemic rice rat <i>Nesoryzomys swarthi</i> and a summary of parasites from both endemic and invasive rodents		● (12) <u>Zoe Von Holten</u>, T.J. Odom, Olivia Chapman, Bryan McLean, Rokeya Ahmed, Stephen Greiman Seasonal patterns in metacommunity structure of tapeworms from <i>Sorex</i> shrews in North Carolina

2:30–3:00 pm

Coffee Break

Alcoves Level 2

3:00–4:00 pm

Sessions IIA & IIB

Session IIA: Taxonomy & Systematics 2 Salon 9/10		Session IIB: Chemotherapy Salon 11/12	
Presiding: Veronica Bueno (University of Connecticut)		Presiding: Damien O'Halloran (George Washington University)	
3:00 pm	● (13) <u>Rokeya Ahmed</u>, Stephen Greiman, Dmitry Apanaskevich Integrating mitogenomic and morphological data for the identification of <i>Hyalomma</i> tick species, vectors of Crimean–Congo Hemorrhagic Fever Virus	● (17) <u>Elise McKean</u>, Young-Jun Choi, Makedonka Mitreva, Damien O'Halloran, John Hawdon Contrasting genomic signatures of benzimidazole and macrocyclic lactone resistance in <i>Ancylostoma caninum</i>	
3:15 pm	● (14) <u>Daniel Gordillo-González</u>, Kamila Cajiao-Mora, John Brule, Santiago Escobar-Alfonso, Micah Warren, Triet Truong, Stephen Curran, ... Stephen Bullard Black bass gill lice: Taxonomy and genetics of <i>Achtheres micropteri</i> Wright, 1882 (Copepoda: Lernaeopodidae) infecting largemouth bass, <i>Micropterus salmoides</i> and spotted bass, <i>Micropterus punctulatus</i> in Alabama and North Carolina	● (18) <u>Adam Ajisere</u>, Silvia Moreno, Daniel Abugri Screening and repurposing of antifungal compounds against <i>Toxoplasma gondii</i>	
3:30 pm	(15) <u>Micah Warren</u>, Stephen Bullard A new species of blood parasite infecting black basses (<i>Micropterus</i> spp.) from the Coosa River, Alabama	● (19) <u>Kathryn Beebe</u>, Lamba Sangare The FDA-approved medication sertraline impairs <i>Toxoplasma gondii</i> replication and induces cyst formation in infected host cells	
3:45 pm	(16) <u>Sara Brant</u>, Pablo Oyarzun-Ruiz New taxa illustrate emerging biogeographic patterns of avian schistosomatids (Schistosomatidae: Digenea)	(20) <u>Catherine Jackson</u>, Matthew Zincone, Emily Mevers, Andrew Lowell, John Hawdon Bioactive terpene isolated from <i>Momordica charantia</i> plant exhibits potent activity against larval and adult <i>Ancylostoma</i> species	

4:00–5:00 pm

President's Symposium

Ballroom D

Quo vadis, ASP?: An interactive symposium on the future of the society	
Presiding: Anindo Choudhury (St. Norbert College)	
4:00 pm	Opening remarks
4:05 pm	Open forum
4:50 pm	Closing remarks

Sunday, 26 July 2026

5:00–6:00 pm

President’s Address

Ballroom D

Presiding:
Kelly Weinersmith (Rice University)

5:00 pm Kelly Weinersmith
Introduction of President Anindo Choudhury

5:10 pm Anindo Choudhury, President
A gut feeling about it: The enigma of the human broad tapeworm



6:30–9:00 pm

Welcome Reception

Ballroom C/Ballroom Foyer

Monday, 27 July 2026

● student presentation in the Best Student Presentation Competition

7:30 am–5:00 pm

Registration

Ballroom Foyer, Desk C

8:30–10:00 am

Sessions IIIA & IIIB

Session IIIA: Ecology 2 Salon 9/10		Session IIIB: Host-Parasite Interactions 1 Salon 11/12	
Presiding: Lauren Camp (University of Wyoming) Seth Bromagen (Columbia College)		Presiding: Brandon Ruehle (Peru State College) Graham Goodman (Utah State University)	
8:30 am		● (27) <u>Briana Zaffiro</u> , Christopher Blamar, David Kerstetter, Eloy Martinez Thermal preferences of bivesiculid cercariae	
8:45 am	(22) Valeria Pobirohin, Abigail Finch, Ness Dalling, <u>Jillian Detwiler</u> Extending the lack of evidence for manipulation: No effect of <i>Parelaphostrongylus</i> spp. on the behaviour of 2 gastropod intermediate host species	● (28) <u>Juliette Rodrigue</u> , Matthew Atkinson Pathogenic infection minimally impacts body condition and immune response in free-ranging Cuban treefrogs, <i>Osteopilus septentrionalis</i> , in central Florida, USA	
9:00 am	● (23) <u>Chiara Rizzuti</u> , Armand Kuris, Kevin Lafferty, Ryan Hechinger Food-web exploiting parasites dominate parasitic load and diversity in Pacific jackknife clams (<i>Tagelus</i> spp.)	● (29) <u>Sydney Horan</u> , Janine Caira, Timothy Moore, Eric Bae Using historical parasite collection data to reconstruct avian host biology	
9:15 am	● (24) <u>Brooklyn Minton</u> , Melanie Langford, Allison Durland-Donahou, Gabriel Langford There and back again: Discovering the complex life cycles of bull shark (<i>Carcharhinus leucas</i>) tapeworms	● (30) <u>Ryne Maness</u> , Charles Criscione Fit/fat, or full of parasites? Associations between body fat and helminth infection in an invasive gekkonid	
9:30 am	● (25) <u>Irvin Arroyo-Torres</u> , Thomas Turner, Lisa Barrow, Layla Denee, Grace Carmona-Yong, Takuma Shiina, Ariadna Torres, ... Sara Brant Assessing environmental and biotic drivers of parasite assemblages across hosts through time in arid-land streams using museum specimens	● (31) <u>Hayden Krause</u> , Sascha Hallett Assessing the risks of <i>Sanguinicola</i> sp. to juvenile spring-run Chinook salmon (<i>Oncorhynchus tshawytscha</i>), following Klamath River Dam removal	
9:45 am	● (26) <u>Sasha Sypher</u> , Armand Kuris, Kevin Lafferty, Ryan Hechinger The striped shore crab (<i>Pachygrapsus crassipes</i>) is loaded with diverse parasites that mostly transmit to bird, fish, and shark/ray predators	● (32) <u>Alexa Todd</u> , Daniel Lindo, Julia Whale, Jessica Rotolo, John Barta Intestinal parasites in cats entering local animal shelters in southern Ontario	

10:00–10:30 am

Coffee Break

Alcoves Level 2

Monday, 27 July 2026

10:30–Noon

Sessions IVA & IVB

Winston 1C

Session IVA: Taxonomy & Systematics 3 Salon 9/10		Session IVB: Host-Parasite Interactions 2 Salon 11/12	
Presiding: Kaylee Herzog (University of New Mexico) Katherine Hanselman (University of Kansas)		Presiding: Charles Criscione (Texas A&M University, College Station) Chelsea Thorn (Texas A&M University, College Station)	
10:30 am	● (33) <u>Felix Berrios Ortega</u>, James Bernot Development of an open-access interactive key for <i>Lepeophtheirus</i> (Copepoda: Caligidae) based on original type descriptions and CLSM redescrptions	10:30 am	● (39) <u>Stephanie Martinez-Beltran</u>, Caroline de Moraes de Siqueira, Jeroen Saeij GRA70 enhances parasite fitness during IFNγ restriction of <i>Toxoplasma gondii</i>
10:45 am	(34) <u>Christine Smith</u>, Stephen Curran, Haley Dutton, John Brule, Daniel Gordillo-González, Santiago Escobar-Alfonso, Triet Truong, ... Stephen Bullard Taxonomy and parasitology of some viviparid snails from Alabama and Arkansas	10:45 am	● (40) <u>Erik Hatlestad</u>, Ben Hanelt Impact of the hairworm <i>Paragordius varius</i> infection on the fecundity of physid snails
11:00 am	(35) James Bernot A target capture probe set for copepod phylogenomics	11:00 am	● (41) <u>Beka Raya Abagero</u>, Franck Dumetz, Tirusew Tolosa, Daniel Tesefay, Tassew Shenkutie, Biniyam Lukas, Delenesaw Yewhalaw, ... Eugenia Lo Short-term <i>ex vivo</i> culture reshapes developmental composition and selectively filters <i>Plasmodium vivax</i> haplotypes
11:15 am	(36) <u>Tyler Achatz</u>, Zoe Von Holten, Makala Fabrizio, Theophilus Amporful, Stephen Greiman, Kari Waddle, Nichole Carpenter, ... Vasyl Tkach Detection of new <i>Posthodiplostomum</i> spp. (Digenea: Diplostomoidea) from the New World	11:15 am	● (42) <u>Dawood Abbas</u>, Lamba Sangare Distinct HIF-1α signaling pathway in syncytiotrophoblasts mediates the restriction of <i>Toxoplasma gondii</i> replication
11:30 am	● (37) <u>Kamila Cajiao-Mora</u>, Stephen Curran, John Brule, Daniel Gordillo-González, Haley Dutton, Micah Warren, Stephen Bullard Identical life cycles in two American alligator trematodes, <i>Proctoacaecum diploporum</i> and <i>Proctoacaecum coronarium</i>, from coastal Alabama	11:30 am	● (43) <u>Beth Cohen</u>, Parryrn Kruth, John Barta Temperature-responsive mRNA as a molecular marker of oocyst viability in <i>Eimeria</i> spp. using RT-qPCR
11:45 am	(38) John Hnida Local fauna as a key resource for advancing coccidian taxonomy (and one's career)	11:45 am	(44) Lucy Fry, Het Adhvaryu, Hayden Roys, Anne Bowlin, Gopinath Venugopal, Jordan Bird, Charity Washam, ... <u>Tiffany Weinkopff</u> Guanylate-binding proteins balance iNOS/Arg-1 in myeloid cells during <i>Leishmania major</i> infection and promote host defense to infection

Noon–1:00 pm

Student Lunch Vortex

Salon 13

1:15–2:45 pm

Sessions VA & VB

Session VA: Ecology 3 Salon 9/10		Session VB: Host-Parasite Interactions 3 Salon 11/12	
Presiding: John Shea (Creighton University) Nicholas Negovetich (Angelo State University)		Presiding: Kristin Herrmann (Tarleton State University) Ben Hanelt (University of New Mexico)	
1:15 pm	● (45) <u>Connor McCowan</u> , Christina Anaya Comparing the parasite fauna of invasive cane toads and native southern toads within Florida ecosystems	(51) <u>Valerie McKenzie</u> , Timothy Korpita	Field probiotic treatment reduces fungal pathogen load on wild boreal toads during metamorphosis
1:30 pm	● (46) <u>Delaney Long</u> , Florian Reyda, Jessica Best A survey of parasites of <i>Morone saxatilis</i> (striped bass) in the Hudson River, New York	(52) <u>Daniel Abugri</u> , Homa Sharma, Japhet Kamasah, Alexandra Richard, Mia Smith, Jesse Kang, Hutton Koehne, ... Emmanuel Tadjuidje	<i>Xenopus laevis</i> larva as novel model for <i>Toxoplasma gondii</i> infection
1:45 pm	● (47) <u>Allison Bryant</u> , Gabriel Langford, Matthew Bolek The first North American evaluation of parasite diversity and their component community structure in invasive tropical house geckos, <i>Hemidactylus mabouia</i> , from Florida	(53) Sonja Olson, Bailey Stuart, Declan Algrem, <u>Nicolas Wheeler</u>	Extraocular color discrimination by <i>Schistosoma mansoni</i> miracidia
2:00 pm	● (48) <u>Sarah Sargent</u> , David Kerstetter, Joanna Cielocha, Christopher Blonar Surveys of <i>Hypanus sabinus</i> and <i>H. say</i> parasites in the Indian River Lagoon estuary, Florida	(54) Eleanor Pace, <u>Michael Zimmermann</u>	The impact of eutrophication on parasite diversity in two isolated ponds at the Huston-Brumbaugh Nature Center
2:15 pm	● (49) <u>Michaela Barnhill</u> , Gabriel Langford, Betsie Rothermel, Rachel Fedders Gastrointestinal parasites of gopher tortoises	(55) <u>Dana Calhoun</u> , Anna Poslednik, Jasmine Groves, William Keeley, Pieter Johnson	The perfect storm: Using camera traps, dissections, and precipitation to understand parasite epizootics
2:30 pm	● (50) <u>Alexia Hilber</u> , David Kerstetter, Christopher Blonar Endoparasite communities of wading and marsh birds in southern Florida	(56) Lijun Lu	Comparative transcriptomic responses to <i>Schistosoma mansoni</i> of two <i>Biomphalaria</i> taxa from Lake Victoria, Kenya: <i>B. sudanica</i> and <i>B. choanomphala</i>

2:45–3:15 pm

Coffee Break

Alcoves Level 2

Monday, 27 July 2026

3:30–4:30 pm

Eminent Parasitologist Lecture

Ballroom C

Presiding:

Susan Perkins (The State University of New York at Potsdam)

3:40 pm

(57) Janine Caira (University of Connecticut)

Recipient of the **Eminent Parasitologist Lectureship**

The wonderful world of tapeworms

4:30–5:30 pm

Business Meeting (open to all; student attendance encouraged)

Ballroom C

Presiding:

Anindo Choudhury (St. Norbert College)

Tuesday, 28 July 2026

● student presentation in the Best Student Presentation Competition

7:30–11:00 am

Registration

Ballroom Foyer, Desk C

8:30–10:00 am

Sessions VIA & VIB

Session VIA: Evolution		Salon 9/10	Session VIB: Ecology 4		Salon 11/12
Presiding:			Presiding:		
James Bernot (University of Connecticut)			Nicholas Wheeler (University of Wisconsin-Eau Claire)		
Felix Berrios Ortega (University of Connecticut)			Reginald Blaylock (University of Southern Mississippi)		
8:30 am	(58) <u>Kaylee Herzog</u> , Zach Pella, Halie Smith, Dayna McCormick, Lily Nuss, Amanda Brinkworth, Sujata Chaudhari, ... Joseph Fauver	When clades collide: Genomic admixture in black-legged ticks (<i>Ixodes scapularis</i>) from the Great Plains	(64) <u>Ben Hanelt</u> , Rachel Swanteson-Franz	Stretching the truth: Length increase in hairworms post host-emergence	
8:45 am	(59) Sydnie McMahan, Noraida Martínez-Rivera, <u>Kirsten Jensen</u>	A comparative investigation of tegumental structures and neuromuscular in three cercarial morphotypes from physid snails from Kansas	(65) Kristin Herrmann	Castration comeback: Evidence of post-infection reproduction in a snail host	
9:00 am	(60) <u>Jessica Rotolo</u> , John Barta	An assessment of the host-specificity of <i>Eimeria</i> species isolated from four galliform birds (chickens, turkeys, northern bobwhites and chukar partridges)	(66) <u>Graham Goodman</u> , Madison Patch, Alex Jones, Sara Weinstein	Worms in the Wild West: Parasite community structure and host condition in feral horses	
9:15 am	(61) Hsuan-Wien Chen	Helminth parasites and their snakehead fish hosts in native and invaded ranges	(67) Jake Metzger, <u>Michael Zimmermann</u>	The role of <i>Posthodiplostomum</i> spp. in the maintenance of a subordinate mating strategy of bluegill sunfish (<i>Lepomis macrochirus</i>)	
9:30 am	(62) Kate Sheehan	Flight fuel and feces: Microbiome dynamics during shorebird stopover	(68) Naresh Kumar Shah	Prevalence of gastrointestinal parasites in goat (<i>Capra hircus</i>) of Malarani Rural Municipality, Arghakhanchi District of Nepal	
9:45 am	(63) <u>Matthew Bolek</u> , Alex Bell, Ben Hanelt, Sara Brant, Agustín Jiménez	The anuran tadpole host as a matchmaker for helminth microbiome symbiotic relationships	● (69) Ana Ardelean, <u>Alexander Olariu</u> , Gheorghe Darabus, Tudor Olariu	Seroprevalence and risk factors associated with <i>Toxoplasma gondii</i> in individuals from Romania with professional exposure	

10:00–10:30 am

Coffee Break

Alcoves Level 2

Tuesday, 28 July 2026

10:30 am–Noon

Sessions VIIA & VIIB

Session VIIA: Genomics		Salon 9/10	Session VIIB: Ecology 5	Salon 11/12
Presiding: Michael Zimmermann (University of Mount Union) Micah B. Warren (Auburn University)			Presiding: F. Agustín Jiménez (Southern Illinois University) Kate Sheehan (Frostburg State University)	
10:30 am	● (70) <u>Chelsea Thorn</u> , Charles Criscione <i>In silico</i> excretory/secretory protein annotation of <i>Oochoristica javaensis</i> , a cyclophyllidean cestode that parasitizes reptiles		(76) <u>Dana Calhoun</u> , Jasmine Groves, Tyler Achatz, John Kinsella, Stephen Greiman, Maggie Young, Rokeya Ahmed, ... Pieter Johnson No free rides: Testing migration-parasite hypotheses across a long-distance migrant	
10:45 am	(71) John Barta Organizational diversity of mitochondrial genomes in adeleorinid and eimeriorinid coccidia (Apicomplexa, Eucoccidiorida)		(77) <u>Richard Clopton</u> , Sierrah Vermeer, Debra Clopton, Jon Kolman Prevalence of Chagas disease (<i>Trypanosoma cruzi</i>) in southeastern Nebraska shelter dogs	
11:00 am	(72) Lucy Fry, Flavia Neto de Jesus, Matheus Batista Carneiro, Hayden Roys, Anne Bowlin, Nathan Peters, Pierre-Yves von der Weid, <u>Tiffany Weinkopff</u> Dysregulated lymphatic remodeling promotes immunopathology during non-healing cutaneous leishmaniasis		(78) <u>Ryan Koch</u> , Kevin Niedringhaus, Andrew Di Salvo, Justin Brown, Roderick Gagne Hunting for <i>Histomonas</i> : Surveillance of birds and their nematodes from Pennsylvania, USA	
11:15 am	(73) <u>Miya Moon</u> , Daniel Abugri Using metabolomics and lipidomics approaches to deciphering apigeninidin chloride mechanism of action		(79) <u>Emily Durkin</u> , Liza Walker, Kathleen Gillis, Carlos Santamaria, John Ambrosio First record of <i>Saccularina</i> sp. in Florida ladyfish (<i>Elops saurus</i>)	
11:30 am	(74) <u>Jazmyn Greggs</u> , Homa Sharma, Daniel Abugri Ionophore (A23187) alteration of <i>Toxoplasma gondii</i> whole lipidome		(80) Christina Anaya When worms wander: Citizen science reveals hair-worms on the move in Florida	
11:45 am	(75) <u>Abdelmalek Lekired</u> , Coen Adema, Si-Ming Zhang A systems-level comparative analysis of global gene expression of resistant and susceptible <i>Biomphalaria glabrata</i> in response to <i>Schistosoma mansoni</i> infection		(81) Hsuan-Wien Chen Helminth parasites of two invasive lizards, the green iguana (<i>Iguana iguana</i>) and the Chinese water dragon (<i>Physignathus cocincinus</i>), in Taiwan	

Noon–1:00 pm

Journal of Parasitology Editorial Luncheon (by invitation only)

Salon 13

1:00–2:00 pm

Students' Symposium

Salon 9/10

What to do after grad school: How to survive as an early career professional Organizer & presiding: Zoe Von Holten (Georgia Southern University), ASP Student Representative	
1:00 pm	Opening remarks
1:05 pm	(82) Matthew Atkinson Staring into the void: Finding opportunities for research in non-tenure track roles in academia
1:30 pm	(83) F. Agustín Jiménez Introspection as a guiding force in career development
1:55 pm	Closing remarks

- student presentation in the Best Student Presentation Competition

2:00–4:00 pm

Poster Session
(incl. Coffee Break and Palettes & Parasites)

Ballroom D

Poster I: Chemotherapy & Drug Resistance/Physiology

- (90) Purvesh Kadam, Jacob Wragge, Jorrico Suelto, Sudhanva Kashyap

SLO-1 regulation determines emodepside sensitivity in *Caenorhabditis elegans*

- (91) Shruti Gupta, Jacob Wragge, Sudhanva Kashyap

Cholinergic tachyphylaxis – convergence or independence of L-AChR machinery and ER protein?

- (92) Julian Garcia, Jacob Wragge, Jorrico Suelto, Sudhanva Kashyap

Towards better schistosomiasis treatment: Pharmacological characterization of the *Sma*-SLO-1 BK channel

- (93) Briana Zaffiro, Christopher Blonar, David Kerstetter, Eloy Martinez

Long-term survival of bivesiculid cercariae in different culture media

Poster II: Epidemiology

- (94) Cassidy Landis, Madison Eshleman, Maiya Singer, Cassandra Seminoff, Gideon Schamberger, Cory Petter, Kimberly Tucker, Matthew Tucker

qPCR-based vector-borne pathogen detection in field-collected Maryland ticks and ticks from white-tailed deer carcasses

- (95) Lauren Reinfeld, Nicholas Mill, Cassandra Seminoff, Jesu Valencia, Maiya Singer, Cory Petter, Cassidy Landis, ... Matthew Tucker

Molecular surveillance of zoonotic and wildlife apicomplexan parasites in Maryland white-tailed deer sampled at managed hunts

- (96) Gideon Schamberger, Cassidy Landis, Matthew Tucker

Molecular identification of tick-borne pathogens in *Ixodes scapularis* from Monroe County, New York

- (97) Molly Deinhart, Kate Sheehan

Predator-parasite interactions and their implications for aquaculture health and sustainability

Poster III: Ecology

- (98) Alexandria Nelson, Abigail Finch, Victor Shr, Jeff Beane, Michael Cove, Kenzie Pereira, Skylar Hopkins

Comparison of *COI* and *28S* metabarcoding to traditional parasitological methods for four snake taxa

- (99) Lydia Hughes, Nancy Smith, William Szelistowski, Micah Bakenhaster

Marine ectoparasite communities on batoid hosts

- (100) Abigail Arnashus, O. Alejandro Aleuy

First report of *Kiricephalus coarctatus* (Pentastomida) in the eastern mud snake (*Farancia abacura*) from Florida

- (101) Oliver Jensen, John Shea, Sudhanva Kashyap

Impact of triazicide and atrazine on adult *Paragordius varius*

- (102) Christopher Blonar, David Marcogliese

Quantifying observer effects in parasite community data

- (103) Isabella Cimino, Elliana Euclide, Kevin Stover, Elizabeth Hoffeditz, Alexander Hernandez

Helminth parasite diversity in white suckers across stream ecosystems in Southeast Pennsylvania

- (104) Elizabeth Bevis, Kate Sheehan

A quantitative assessment of ingested microplastic impact on internal parasites in waterbirds

● (105) Eric Jergensen, Kate Sheehan

Plastics, poisons, and parasites: The impacts of microplastics on endoparasites in eastern newts

● (106) Ema Nagel, Christopher Blamar, David Kerstetter

Gastrointestinal endoparasite communities of wood-warblers in coastal southeast Florida

● (107) Tyler Achatz, Maggie Young, Zoe Von Holten, Makala Fabrizio, Caley Chun, Tyler Harris, Nathaniel Hornung, ... Vasyl Tkach

A survey of endohelminths of holosteans in Georgia

(108) John Shea, Ming-Chung Chiu

Examining altered behavior in millipedes (*Spirobolus* sp.) infected with terrestrial hairworm, *Gordius chiashanus*

(109) Raymond Allen, Gretchen Gerrish

"Can I eat this?": Assessing freshwater fish parasites in the Wisconsin Ceded Territory

(110) Mia Clement

Intestinal parasite communities of invasive cane toads and native southern toads in southwest Florida

(111) Carl Keiser

The Spider Parasite Digital Research (SPDR) Collection

(112) Ash Hernandez-Trochez, Malia Tinsley, Oscar Johnson

Necropsy and specimen curation: A parasitological survey of Florida avifauna

● (113) Luke Niemann

Species survey of helminth parasites from invasive and native snakes in south Florida

● (114) Emma Ulseth, Jordan Donini, Matthew Atkinson

A comparative analysis of body condition and immunomodulation as indicators of stress in native and non-native cane toads (*Rhinella horribilis*)

● (115) Elliana Euclide, Elizabeth Hoffeditz, Alexander Hernandez

Variabilities in host body size and the abundance of *Lissorchi* *attenuatus* in white suckers from tributaries of the Schuykill River watershed

Poster IV: Host-Parasite Interactions

● (116) Madison Eshleman, Cory Petter, Mia Kroll, Karis Dawson, Kasey Burchfield, Matthew Tucker

The use of zero valent iron to bind coccidian parasites and magnetic attraction to remove oocysts from water

● (117) Alex Bell, Matthew Bolek

Seasonal reproductive strategies and occurrence of symbiotic bacteria on *Gyrinicola batrachiensis* (Walton, 1929) infecting green frog tadpoles, *Rana clamitans* (Latreille, 1801) from Wisconsin

● (118) Jake Lighthall, O. Alejandro Aleuy

Beyond presence/absence: A framework for classifying pathogen relevance to mortality in stranded odontocetes

● (119) Blair Willse, Scott Markwith, O. Alejandro Aleuy

Environmental drivers and implications of *Perkinsus marinus* infection in the eastern oyster in southeast Florida

Poster V: Genomics

● (120) Kevin Zhou-Hackbarth, Tibeb Mekonen, Eric Haag, Julie Dunning Hotopp

Conservation and divergence on the neo-Y chromosomes of *Brugia* and *Wuchereria* filarial nematodes

(121) Suk Yul Jung, Seyoung Yang, Eun-Jung Kim

Proteomic changes in *Naegleria fowleri* induced by lectin-glycoproteins

- (122) Dominick Ebaugh, Cristen Rosch, Alexander Hernandez

Impact of habitat fragmentation on the population genetics of *Lissorchis attenuatus* infecting white suckers from Pennsylvania streams

- (123) Amy Gudmundson, Abigail Finch, Jillian Detwiler

Using mitogenome analysis of the *Echinostoma trivolvis* species complex to find echinostome trematode barcoding genes

- (124) Marissa Ohran, Rokeya Ahmed, Stephen Greiman, Dmitry Apanaskevich

Investigating mitogenomic variation in *Haemaphysalis* ticks

Poster VI: Taxonomy Systematics & Phylogeny

- (125) Molly Kennedy, Kirsten Jensen

Whiprays in the genus *Maculabatis* (Elasmobranchii: Urogyrnidae) as hosts of new species of *Caulobothrium* (Cestoda: "Tetraphyllidea") sharing a subtle morphological feature

- (126) Allison Bryant, Gabriel Langford, Matthew Bolek

Histological evaluation of coccidian parasites in the tropical house geckos, *Hemidactylus mabouia* and evidence for a new genus of lizard coccidia

- (127) Matthew Bolek, Allison Bryant, Gabe Langford, Ryan Koch

Do tongueworms (Mandibulata: Pancrustacea) retain two pairs of vestigial antennae? A comparative scanning electron microscopy study

- (128) Tyler Achatz, Brooke Ramsingh, Maggie Young, Jonathon Pritchard, Matthew Keel, Vasyl Tkach

Re-evaluation of *Prohemistomum* and related cyathocotylids (Digenea: Diplostomoidea)

- (129) Nathaniel Hornung, Maggie Young, Tyler Achatz, Rafe Brown, Vasyl Tkach

Exploring the phylogenetic affinities of microcoeliids with preacetabular testes

- (130) John Brule, Kamila Cajiao-Mora, Daniel Gordillo-González, Santiago Escobar-Alfonso, Matthew Horton, Kelly Wittingham, Stephen Bullard

First report of a monogenoid infecting bighead carp, *Hypophthalmichthys nobilis* (Richardson, 1845) (Cypriniformes: Xenocyprididae) in the United States with phylogenetic analysis and inventory of parasites infecting invasive fishes in the United States

Poster VII: Parasite Distributions & New Host Records

- (131) Sydney Horan, Janine Caira

Expanded records of North American avian cyclophyllideans

- (132) Eleni Ryzcek, Christina Anaya

Gastrointestinal parasite community of the invasive brown anole (*Anolis sagrei*) in southwest Florida

- (133) Matthew Stutler, Christina Anaya

When parasites invade the invader: Lung parasites in the Burmese python

- (134) Fernanda Cortazar Penalba, Christina Anaya

Parasite diversity in the southern black racer (*Coluber constrictor priapus*) of southwest Florida

- (135) Noah Lewis, Christina Anaya

Under the scales: A parasite survey of the Mediterranean house gecko in southwest Florida

- (136) Caley Chun, Maggie Young, Jim Page, Matthew Rowe, Caroline Cooper, Laura Wenk, Jonathon Pritchard, ... Tyler Achatz

Determination of rat lungworm hotspots in Georgia

- (137) Jasmine Silvennoinen, Ariel Poholek, O. Alejandro Aleuy

Infection patterns of parasitic isopods in marine fishes in southeast Florida and the Florida Keys

-
- (138) Tajul Islam Mamun, O. Alejandro Aleuy

Echinococcus in Canada and the United States: Multi-host transmission and spatial distribution

- (139) Lauren Camp, Jesalynn Borgman, Katie Bardsley, Ali Brower

Reemergence, or rediscovery, of common liver fluke (*Fasciola hepatica*) in Wyoming, USA

4:00–5:00 pm

Student Business Meeting (for students only)

Salon 9/10

Presiding:

Zoe Von Holten (Georgia Southern University), ASP Student Representative

6:00–6:30 pm

Auction Preview

Ballroom C

6:30–9:00 pm

35th Annual Auction

Ballroom C

Wednesday, 29 July 2026

8:45–9:30 am

Sessions VIIIA & VIIIB

	Session VIIIA: Collections Presiding: Sara Brant (University of New Mexico)	Salon 9/10	Session VIIIB: Host-Parasite Interactions 4 Presiding: Tiffany Weinkopff (University of Arkansas for Medical Sciences)	Salon 11/12
8:45 am	(84) <u>Veronica Bueno</u> , Katrina Menard, Bernard Goffinet, Janine Caira “Infectious” lessons learned from curating problematically preserved parasites		(87) Solomon Jacob, Yetunde Akinbo, Uwem Ekpo, Oluwaremilekun Ajakaye, Zainab Omoruyi, Temitope Agbana, ... <u>Babatunde Osanyinbi</u> , ... Frederick Akinbo Emerging evidence of zoonotic schistosomiasis in humans in Abuja, Nigeria	
9:00 am	(85) <u>Kaylee Herzog</u> , Sara Brant From hosts to history: A behind-the-scenes look at the diverse holdings of the Museum of Southwestern Biology Division of Parasites		(88) <u>Sudhanva Kashyap</u> , Shruti Gupta, Jacob Wragge From paralysis to recovery: Molecular drivers of cholinergic recovery in nematodes	
9:15 am	(86) Anna Phillips Developing a baseline of diversity and specificity of avian cestodes in the Atlantic flyway of North America		(89) <u>Alice Lee</u> , <u>Valerie Lantigua</u> , <u>Mahya Dini</u> , <u>Elizabeth Redman</u> , <u>Taylor Nycum</u> , <u>John Gilleard</u> Frequency and treatment implications of isotype-1 β -tubulin mutations in canine hookworms in Florida	

9:30–10:00 am

Coffee Break

Alcoves Level 2

10:00–11:00 am

H. B. Ward Medal Lecture

Winston 3

	Presiding: Brandon Ruehle (Peru State College)	
10:00 am	John Hawdon (George Washington University) Introduction	
10:10 am	Makedonka Mitreva (Washington University School of Medicine) Recipient of the H. B. Ward Medal Worm DNA and me: A career defined by the genetic code	

11:00 am–12:20 pm

Awards Presentations

Winston 3

Clark P. Read Mentor Award

Presiding:

Brandon Ruehle (Peru State College)

Jessica Rotolo (University of Guelph)

Introduction

John Barta (University of Guelph)

Recipient of the Clark P. Read Mentor Award



Ashton Cuckler New Investigator Award

Presiding:

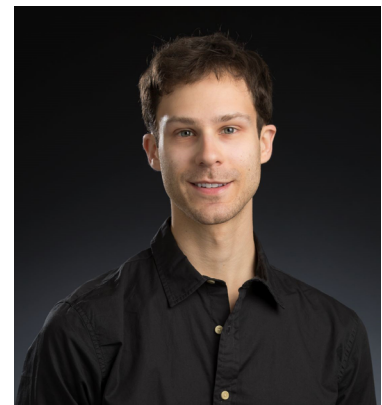
Brandon Ruehle (Peru State College)

Matt Bolek (Oklahoma State University)

Introduction

Ryan Koch (University of Pennsylvania)

Recipient of the Ashton Cuckler New Investigator Award



Best Student Presentation and Mark Dresden Travel Grant Awards

Presiding:

Nicolas Wheeler (University of Wisconsin-Eau Claire)

Best Student Presentation Awards

Mark Dresden Travel Grant Awards

12:20–12:30 pm

Adjournment (& Resolutions &)

Winston 3

See you all next year, July 12–15, 2027 in Auburn, Alabama!

Abstracts

Disclaimer: The authors of the abstracts appearing in this program are solely responsible for the content. These abstracts are for informational purposes only and do not constitute formal publication. They should not be cited as published literature.

1. Temporal analysis of genetic diversity in a multi-host nematode parasite (*Parelaphostrongylus andersoni*) undergoing secondary contact

Abigail C Finch, Jillian T Detwiler

University of Manitoba, Winnipeg, MB, Canada

Climate change and habitat alteration are shifting the ranges of many host species, causing changes in the distributions and potentially the genetic diversity of their parasites. The nematode parasite musclemworm (*Parelaphostrongylus andersoni*) can infect both white-tailed deer and caribou due to a host-switching event that occurred when these host species were sympatric during the Pleistocene. Following the Wisconsin glaciation, caribou retreated northward, out of white-tailed deer range, preventing interbreeding of musclemworm between the two host species. In Manitoba, the recent range expansion of white-tailed deer has led these two host species to overlap once again, providing opportunities for gene flow of musclemworm. Currently, very little is known about the genetic variation of musclemworm. Caribou Management Unit 2, “The Bog,” provides an ideal location to explore how parasite genetic diversity changes over time in response to host range shifts. Both host species are present in this area, with white-tailed deer having arrived around 100 years ago. This study aims to temporally assess the occurrence and genetic diversity of musclemworm in The Bog. To achieve this, caribou and white-tailed deer fecal pellets were collected from The Bog on several occasions from 2006–2026. Nematode larvae will be sedimented from fecal pellets, and DNA will be extracted from individual larva, amplified for the CO1 gene, and sequenced using Sanger sequencing. To genetically identify parasite species, the blastn algorithm will be performed on 798 bp sequences. Network analyses will identify subpopulations of parasites, and the fixation index (FST) will be calculated to estimate genetic differentiation among subpopulations. An AMOVA will be performed to predict genetic variance due to year and host. We expect the genetic differentiation between subpopulations of musclemworm to decrease over time due to increased movement and range overlap of hosts facilitating secondary contact and dispersal. Preliminary results from 2006 indicate that 20/34 pellet groups contained larvae and all sequenced larvae form a subpopulation that is distinct from another subpopulation only found in white-tailed deer in Manitoba (p distance > 3%). Our work will improve our knowledge of the distribution, phylogeography, and temporal genetic diversity of musclemworm.

2. A new genus and species of trematode parasite (Plagiorchiodea: Ochetosomatidae) from the oral cavities of snakes

Alexandria P Nelson¹, Wesley Neely², Cory C McKinstry^{2,1}, Kenzie Pereira¹, Jeff Beane³, David Rodriguez², Skylar R Hopkins¹

¹North Carolina State University, Raleigh, NC, USA. ²Texas State University, San Marcos, TX, USA. ³North Carolina Museum of Natural Sciences, Raleigh, NC, USA

Members of the trematode family Ochetosomatidae Leão, 1945 use snakes as final hosts. This group has been taxonomically debated for nearly 100 years, with 29 genera raised at different times, but only six remaining now. Multiple genera are also synonymous with one another (e.g., *Ochetosoma* Braun, 1901 = *Pseudorenenifer* Price, 1935 = *Neorenenifer* Byrd & Denton, 1938 = *Neochetosoma* Caballero, 1949 = *Renifer* Pratt, 1902). The type genus *Ochetosoma* is perhaps the most highly debated, having over 30 species synonymizations and the interchangeable use of *Renifer* and *Ochetosoma* in the recent literature. *Ochetosoma aniarum* (Leidy, 1891) Dubois & Mahon, 1959 has 11 synonyms, the majority of which were described by Dubois and Mahon (1959), who distinguished *O. aniarum* morphologically from all other *Ochetosoma* by the genital

pore that is located proximal to the oral sucker, vitelline fields divided into two groups (pre- and post-acetabular), and highly developed ventral sucker with sucker ratio 1:1.5. However, we observed a genital pore proximal to the oral sucker and vitelline fields divided into two groups in two distinct oral trematode morphospecies observed during systematic surveys of live *Nerodia* spp. snakes in Texas and live and salvaged dead-on-road (DOR) snakes from North Carolina. Based on these distinct morphological features and our 28S phylogenetic analysis, we determined that these were two morphologically, genetically, and geographically distinct taxa. The first taxon is identical to *O. aniarum* and is found in Texas. The second taxon from North Carolina, which we describe and name here, cannot be definitively assigned to any existing synonym of *O. aniarum*. Furthermore, morphological and genetic evidence suggest that both species are representatives of a new genus, which we diagnose. Freshwater snail surveys and additional DNA sequencing allowed us to describe the first intermediate host stages of the North Carolina species. This study is a step forward in untangling the complicated taxonomy and ecology of the Ochetsomatidae and provides a framework for trematode taxonomists to begin addressing cryptic species in this group.

3. The copepod genus *Eudactylina*: Working towards a stronger grasp of elasmobranch gill parasite systematics

Douglas Stephan¹, Gregory B Deets², James P Bernot¹

¹University of Connecticut, Storrs, CT, USA. ²Independent Researcher, Los Angeles, CA, USA

The family Eudactylinidae is a group of parasitic copepods found on elasmobranchs and teleosts that currently comprises 62 valid species across 12 genera. With 39 valid species, by far the most speciose is the genus *Eudactylina*, a group of small copepods that possess remarkable chelate maxillipeds that they use to grasp the secondary lamellae of the gills of their hosts. The genus is globally distributed and collectively parasitizes the gills of 10 families of sharks and 9 families of batoids. Species of *Eudactylina* exhibit a high degree of morphological similarity but can be differentiated using fine morphological features such as the characteristic cuticular projections found along much of their body and appendages, which can vary in both shape and pattern. Other key taxonomic characters include the structure and setal armature of the caudal ramus and antenna. In the dissertation by Deets (1994), 9 new species of *Eudactylina* were described but they were never formally published. In this study, reexamination of the types of these 9 new species and comparison to the 7 species described since Deets (1994) confirmed all 9 remain undescribed. We are thus formally describing these 9 species and updating their differential diagnoses. Newly generated confocal laser scanning micrographs of the type specimens accompany the new description. In addition, Parsimony and Bayesian Inference phylogenetic analyses are presented for 75 characters scored from 28 species of *Eudactylina*. This work improves our understanding of the morphological diversity of the genus and serves as the foundation for a new key to species of *Eudactylina*. Geographical distributions and host associations of the genus are also discussed.

4. Fretting over guitarfishes: Exploring patterns of diversity of species of *Polypocephalus* (Cestoda: Lecanicephalidea) parasitizing members of the Rhinopristiformes

Katherine M Hanselman, Kirsten Jensen

University of Kansas, Lawrence, KS, USA

Polypocephalus has long been recognized as paraphyletic, and unpublished molecular data suggest the genus is comprised of members of as many as 10 distinct clades, with strong signal for host families and orders. These data also indicate that the diversity of species of *Polypocephalus* parasitizing rhinopristiform elasmobranchs (guitarfishes, wedgefishes, and their allies) is particularly understudied. The focus on rhinopristiforms was further motivated by the Sharpnose guitarfish, *Glaucostegus granulatus*, as host of the type species, *Polypocephalus radiatus*, and by the fact that 5 described species of *Polypocephalus* are currently considered *species inquirendae* and are in need of additional work. We examined tapeworms of 3 of 7 spe-

cies of *Glaucostegus* in the Glaucostegidae (giant guitarfishes), and 2 of 8 species of *Rhynchobatus* and the monotypic *Rhina* in the Rhinidae (wedgetfishes). Morphological examination revealed a recurring pattern across host species: Each rhinopristiform species hosted at least 3 species of *Polypocephalus* representing distinct morphotypes. These included a small form with 4 testes, a scolex narrower than the strobila, and craspedote proglottids; a second small form with 4 testes, a scolex wider than the strobila, and acraspedote proglottids; and a third, typically larger form, 5 mm or longer, whose morphology differed by host family. In glaucostegids, the larger form resembles *P. radiatus*, with 6 testes and craspedote proglottids, while in rhinids, it had 4 testes and a characteristically large cirrus sac. Species of a similar morphotype do not appear to be each other's closest relatives. None of the specimens recovered resembled the 5 species *inquirendae* described from wedgetfishes, suggesting that most, if not all, of the species examined in this study are new to science. Preliminary examination of species in the other rhinopristiform families, Pristidae (sawfishes) and Rhinobatidae (common guitarfishes), suggests that *Polypocephalus* is much less speciose in those groups. Future work will focus on characterizing tentacle-bearing clades to assess whether they can be diagnosed as distinct genera, and on further investigating patterns of host associations and specificity in this group.

5. Discovery of 10 new species expands our concept of morphological diversity in the parasitic copepod genus *Pseudotaeniacanthus*

Netanya Williams, James P Bernot

University of Connecticut, Storrs, CT, USA

The copepod genus *Pseudotaeniacanthus* consists of 11 described species that parasitize the gills and body surface of marine eels, with most species found on morays (Muraenidae). In this study, collections of *Pseudotaeniacanthus* from morays off Japan, Australia, and Vietnam revealed new patterns of morphological variation within *Pseudotaeniacanthus*. Prior to our work, a single species was known to possess an elongate body form. We have identified 10 putative new species of *Pseudotaeniacanthus*, five of which exhibit the elongate body form, indicating the elongate form is much more common than previously recognized. Among these 10 species are several with morphological features not exhibited in any described members of the genus. Two notable examples include the cuticular expansions ornamenting the legs of one new species and the pronged labral furca of another. The vast majority of parasitic copepod taxonomy is based on distinctions in female morphology, but among our newly collected material is a pair of long-bodied species parasitizing *Gymnothorax pseudothyrsoides* in which females are morphologically similar while the males are more easily distinguished, suggesting male morphology may be more useful for delineating species of *Pseudotaeniacanthus* than previously appreciated. We also present a new hypothesis regarding the function of the unusual maxilliped observed in members of this genus. While the maxilliped is typically a clawed appendage that serves as one of the primary attachment structures in parasitic copepods, the maxilliped in *Pseudotaeniacanthus* lacks a claw, making its function unclear. Based on observations with scanning electron microscopy, we hypothesize that this weakly armed appendage may aid in host attachment by helping to form the lateral margins of the cephalothoracic sucker.

6. Helminth parasites of Galápagos mammals: A new cestode of the genus *Raillietina* from the endemic rice rat *Nesoryzomys swarthi* and a summary of parasites from both endemic and invasive rodents

Scott L Gardner¹, Altangerel T Dursahinhan^{1,2}

¹Harold W. Manter Laboratory of Parasitology at University of Nebraska-Lincoln, Lincoln, Nebraska, USA.

²Creighton University, Omaha, Nebraska, USA

In this first report of endoparasites from endemic land-mammals of the Galápagos Islands, we describe a new species of cestode of the genus *Raillietina* (Cyclophyllidae: Davaineidae) from a species of *Nesoryzomys* and summarize the extent of helminth parasitism in both oryzomyine endemics and introduced species of *Rat-*

tus. Up to the current time, no helminth parasites have been reported from rodents of the Galápagos, and little work has yet been done describing and synthesizing Galápagos parasite diversity. In historical times, several species of autochthonous rodents have occupied the islands including: *Nesoryzomys narboroughi* Heller 1904, *N. fernandinae* Hutterer and Hirsch 1979, *N. swarthi* Orr, 1938, and *Aegialomys galapagoensis* (Waterhouse, 1839). Colonization of the islands by humans brought 3 known species of synanthropic rodents: *Rattus rattus*, *R. norvegicus*, and *Mus musculus* which are suspected to have caused the extinction of at least 3 other oryzomyines in historical times.

7. Detection of *Anguillicoloides crassus* (Nematoda) and a survey of endohelminths of American eels in Georgia, USA

Maggie A Young^{1,2}, Makala E Fabrizio¹, Marion Baker³, Jim Page³, Brandon W Baker³, Caroline Cooper³, Amory Cook³, J. Mike Kinsella⁴, Florian B Reyda⁵, Anindo Choudhury⁶, Vasyl V Tkach⁷, Tyler J Achatz¹

¹Middle Georgia State University, Macon, GA, USA. ²University of North Dakota, Grand Forks, ND, USA. ³Georgia Department of Natural Resources, Atlanta, GA, USA. ⁴HelmWest Laboratory, Missoula, MT, USA. ⁵State University of New York at Oneonta, Cooperstown, NY, USA. ⁶St. Norbert College, De Pere, WI, USA. ⁷University of North Dakota, Grand Forks, GA, USA

The American eel *Anguilla rostrata* is a catadromous fish with a unique life history; however, parasite surveys of these eels in the Southeastern USA are limited. In this study, we surveyed the parasite fauna of 98 American eels collected from the Altamaha and Ocmulgee rivers in Georgia between January 2024 and August 2025. Eels were examined for external and internal parasites. The invasive, pathogenic swim bladder nematode *Anguillicoloides crassus* was detected in 62 of 98 eels (63.2% prevalence), with all infections occurring in the Altamaha River population. Infected eels harbored up to 21 nematodes, although most infections consisted of fewer than 5 individuals. No clear seasonal trends of infection were observed. The prevalence and mean intensity of *A. crassus* infections observed in Georgia were higher than those reported for most other regions along the US East Coast. This study provides the first published record of *A. crassus* from Georgia, and expands the known parasite diversity of American eels within the state. Our data also demonstrates the presence of 2 trematode genera, 3 cestode genera, 6 nematode genera, 3 acanthocephalan genera, and 1 arthropod genus. Many of these represent the first reports from eels in the state of Georgia.

8. A bird's-eye view of *Toxoplasma gondii* in New Zealand: Prevalence across hosts, habitats, and ecological traits

Katherine Buschang¹, Robert Poulin¹, Clément Lagrue², Jerusha Bennett¹

¹University of Otago, Dunedin, New Zealand. ²Department of Conservation, Dunedin, New Zealand

Toxoplasma gondii is a globally distributed parasite of increasing concern for wildlife conservation, yet its ecology in avian hosts remains poorly resolved, particularly in New Zealand, where endemic bird communities interact with an introduced definitive host. We conducted a molecular survey of 493 individuals across 29 wild bird species spanning multiple avian orders and ecological niches, using two primer sets to estimate prevalence. *T. gondii* was detected in 39 individuals (7.9%), with positive cases occurring across phylogenetically diverse hosts inhabiting marine, wetland, forest, and human-modified environments. Infection was observed in species representing a broad range of trophic strategies, from herbivores and invertivores to higher-level predators. Despite this ecological diversity, no clear clustering of infection was apparent across major habitat or trophic groupings, suggesting that exposure is not strongly restricted by host type. These findings are consistent with widespread, low-level environmental contamination rather than tightly constrained trophic transmission pathways. This study provides one of the first multi-species baselines for *T. gondii* in New Zealand avifauna and highlights the role of birds as indicators of environmental exposure. Establishing such baselines is critical for assessing the ecological consequences of introduced parasites in isolated ecosystems and for informing conservation monitoring frameworks.

9. Parasites on the urban edge: A review of host–parasite shifts in cityscapes

Jasmine A Groves, Jasmine N Childress

University of Wisconsin - Madison, Madison, WI, USA

As urban areas continue to expand with increasing human populations, animals and their parasites are subjected to changes in habitat and resources. Currently, there are two competing hypotheses to explain how parasite biodiversity will respond to urbanization. Either parasite biodiversity is lower in urban areas because hosts are released from parasite pressure, or parasite biodiversity is higher in urban areas due to increased host densities or exposure to novel parasites. To test whether hosts are more or less parasitized, we have compared parasite biodiversity and prevalence for hosts in their native and urban ranges. We conducted a systematic literature review following the Preferred Reporting Items for Systematic reviews and Meta-Analyses (PRISMA). Using open-source databases, we gathered literature and surveys involving host organisms and their parasite communities in urban landscapes. We recorded information from each manuscript with host species, location, parasite prevalence, and parasite richness. For this review, we narrowed our search to common freshwater hosts of parasites with complex life cycles: molluscs, fish, amphibians, and birds. There have been 56 urban studies that study the prevalence and parasite richness in freshwater hosts found in urban habitats, totaling 36 amphibia, 21 avian, 7 fish, and 5 mollusc different species. Within each taxonomic group, we have compiled more than 200 parasites of amphibians, 112 from avians, 40 from fish, and 12 from molluscs. Interestingly, our preliminary analysis for the amphibia taxon showed that standardized mean richness is significantly higher in urban landscapes (0.72 ± 1.28) compared to natural habitat populations (0.59 ± 0.45) when comparing with a Wilcoxon signed-rank test ($W = 4963.5$; $p = 0.0435$). Mean and summed prevalence of parasites, however, was non-significant ($W = 4718$, $p = 0.2954$; $W = 4342.5$, $p = 0.05279$). This suggests that urban habitats could increase parasite diversity in hosts, but not the burden of infection. We can use this meta-analysis to generalize patterns for how urbanization shapes parasite diversity and prevalence. This work can broaden the field of parasite ecology by establishing life-cycle patterns and generating a predictive framework to understand how growing urbanization will restructure host-parasite dynamics.

10. Surveillance of *Heterobilharzia americana* in recreational water bodies of the Colorado River basin: Implications for canine health

Connor J Goldy¹, Anil Baniya¹, Perla Achi¹, Cullen McCarthy¹, Adler Dillman¹, Lanie Bavier¹, Robert Pena¹, Daphane Mendez¹, Kielee Courts¹, Virginia Li¹, Riley Rackliffe²

¹UC Riverside, Riverside, CA, USA. ²NPS, Boulder City, AZ, USA

Here is an example of the corrected, tightened version that fixes the parasitology error, closes the loop on the molecular data, and uses strong active voice. Be sure to apply the italics where needed before submitting: The parasitic schistosome *Heterobilharzia americana* poses a severe health threat to canines and other mammals, and its geographic range appears to be expanding within the southwestern United States. Building on our prior discovery of the parasite in the Colorado River, we mapped the spatial distribution of *H. americana* across recreational water bodies associated with the Colorado River basin and surrounding regions, including sites in California, Arizona, Nevada, and Utah. A total of 10 recreational sites were surveyed across two field seasons (2024–2025), comprising reservoirs, rivers, and shoreline habitats. We collected known intermediate hosts (*Galba* spp.) and co-occurring snail taxa to assess host range, alongside raccoon (*Procyon lotor*) fecal samples. We detected *H. americana* via observation of cercarial shedding in snails, microscopic identification of eggs in feces, and targeted PCR amplification of the cytochrome c oxidase subunit 1 (*cox1*) gene, followed by Sanger sequencing for species confirmation. Across both seasons, 3,121 snails representing 17 species were collected. *H. americana* infections were detected exclusively in *Galba* spp., with 3 of 566 *Galba* snails (0.53%) actively shedding cercariae (all from 2024 collections). Furthermore, 32 of 49 raccoon fecal samples (65.3%) contained *H. americana* eggs, confirming their role as natural reservoir hosts. Sanger sequencing successfully confirmed *H. americana* identity across both snail and raccoon samples. Our results support multiple hypotheses for snail-mediated parasite dispersal, including hydrological

connectivity, human-mediated transport, and avian-mediated dispersal along migratory flyways. Together, these results demonstrate widespread *H. americana* presence across high-use recreational environments. Combined with the high prevalence of infection in local raccoons, these data indicate a substantial, under-recognized risk of canine exposure in the southwestern United States.

11. Molecular detection of White Spot Syndrome Virus (WSSV) and Yellow Head Virus (YHV) in wild-caught northern brown shrimp (*Farfantepenaeus aztecus*), northern white shrimp (*Litopenaeus setiferus*), and rough mantis shrimp (*Squilla empusa*) from the Gulf of America

Santiago Escobar-Alfonso, John H Brule, Stephen A Bullard

Auburn University, Auburn, AL, USA.

White Spot Syndrome Virus (WSSV), Yellow Head Virus (YHV), and Infectious Myonecrosis Virus (IMNV) comprise demonstrable pathogens in shrimp aquaculture globally but their distribution in nature and occurrence among wild shrimps is less studied. Herein, we used conventional PCR assays to opportunistically surveil for these viruses among wild shrimp specimens that were captured by trawl in the Gulf of America during the 2025 Summer Bottom Groundfish Survey conducted by the National Oceanic and Atmospheric Administration's (NOAA) National Marine Fisheries Service (NMFS). A total of 90 shrimp specimens were sampled and processed for virology herein: 56 brown shrimp (*Farfantepenaeus aztecus*), 24 white shrimp (*Litopenaeus setiferus*), and 10 rough mantis shrimp (*Squilla empusa*). Muscle tissue was collected for DNA and RNA extractions and screened for WSSV, YHV, and IMNV. Of 90 shrimp specimens examined, 11 were positive for WSSV (8 northern brown shrimp [9%] + 3 northern white shrimp [3%]) and 4 were positive for YHV (3 northern brown shrimp [3%] + 1 mantis shrimp [1%]). This is the first record of an infection by YHV in a wild Gulf of America shrimp.

12. Seasonal patterns in metacommunity structure of tapeworms from *Sorex* shrews in North Carolina

Zoe S Von Holten¹, TJ Odom², Olivia S Chapman³, Bryan McLean³, Rokeya Ahmed¹, Stephen E Greiman¹

¹Georgia Southern University, Statesboro, GA, USA. ²University of Georgia, Athens, GA, USA. ³University of North Carolina, Greensboro, NC, USA

Shrews in the genus *Sorex*, found across North America and Eurasia, host a great diversity of Cyclophyllidean tapeworms from the Family Hymenolepididae; in total there are 14 genera known in North America. Despite notably high parasite diversity and wide distribution, comprehensive sampling efforts to document parasites of *Sorex* spp. are rare in the Southeastern USA. To date, only 1 study has been done in North Carolina, finding a diverse community of 7 cestode genera. The present study aimed to understand metacommunity dynamics of tapeworms from Coweeta Hydrologic Laboratory in Macon County, North Carolina within *Sorex* shrews in response to biotic (host species, sex, reproductive class) and abiotic (precipitation, temperature, elevation) factors. Hosts and parasites were collected in Winter, Spring, Summer and Fall of 2025. Cestodes were sorted in the lab and identified based on both morphology and 28S rDNA sequences and counted to obtain abundance data. Elements of Metacommunity Structure (EMS) framework was implemented in R, followed by a Generalized Boosted Regression Model to determine the relative influence of the ecological or host-associated explanatory variables on cestode metacommunity structure. So far, we have documented 6 tapeworm species across 4 different genera using combined morphological and genetic data, though total diversity likely includes 3 additional genera based on morphology. The mean abundance of tapeworms varied seasonally and ranged from 633 (0–13,543) worms per host in the Spring to 131 (0–610) worms per host in the Summer. Cestode infections were overwhelmingly common, with only 7 out of 114 individuals being found with 0 tapeworms. Preliminary metacommunity analyses suggest complex interactions of abiotic and biotic factors in structuring shrew cestode communities.

13. Integrating mitogenomic and morphological data for the identification of *Hyalomma* tick species, vectors of Crimean–Congo Hemorrhagic Fever Virus

Rokeya Ahmed, Stephen E Greiman, Dmitry A Apanaskevich

Georgia Southern University, Statesboro, GA, USA

Hyalomma ticks are important vectors of zoonotic and veterinary pathogens throughout Africa, the Middle East, southern Europe, and Asia, including the Crimean–Congo hemorrhagic fever virus (CCHFV), the causative agent of a severe disease with a high fatality rate in humans. Accurate species identification within this genus remains challenging due to strong morphological similarity among closely related taxa and frequent misidentifications. Therefore, we are trying to establish molecular comparison using newly generated mitochondrial genome (mitogenome) data from multiple *Hyalomma* specimens collected across diverse geographic regions, including East, West, and Southern Africa (e.g., Kenya, Tanzania, Nigeria, South Africa, Namibia); the Middle East and Central Asia (e.g., Iraq, Saudi Arabia, Turkmenistan); South Asia (Pakistan, Sri Lanka); and southern Europe (e.g., Spain, Portugal, Italy). These molecular data are complemented by detailed morphological examinations. Comparative analyses of mitogenomic sequences provide insights into genetic divergence and relationships among key taxa, while morphological assessments highlight both conserved and diagnostic characters. Our results demonstrate the utility of combining mitogenomic data with traditional morphology to improve species-level resolution within *Hyalomma*. This integrative approach contributes to more reliable identification of epidemiologically important species and supports ongoing efforts in tick systematics and vector surveillance.

14. Black bass gill lice: Taxonomy and genetics of *Achtheres micropteri* Wright, 1882 (Copepoda: Lernaepodidae) infecting largemouth bass, *Micropterus salmoides* and spotted bass, *Micropterus punctulatus* in Alabama and North Carolina

Daniel Gordillo-González, Kamila Cajiao-Mora, John H Brule, Santiago Escobar-Alfonso, Micah B Warren, Triet N Truong, Stephen S Curran, Haley R Dutton, Christine M Smith, Stephen A Bullard

Auburn University, Auburn, AL, USA

The “gill lice” *Achtheres micropteri* Wright, 1882 and *Achtheres pimelodi* Krøyer, 1863 (Copepoda: Lernaepodidae) reportedly infect buccal cavity and “gill” of several species of black basses (Centrarchiformes) and catfishes (Siluriformes), respectively. Both of these lernaepodids need to be reassessed morphologically and genetically: their original descriptions are incomplete, their type hosts ambiguously assigned or indeterminate, type specimens not deposited or never assigned, existing vouchers at Smithsonian are not available for dissection (making species-level identification impossible as the original description is based on morphology only), the synonymy that collapsed these species was unjustified and over-generalized, no useful nucleotide sequences exist for either species, and nucleotide sequences representing the diversity of accepted species of *Achtheres* are few (none represented a North American species of *Achtheres* previously). Herein, we provide a supplemental description of *A. micropteri* based on newly collected specimens from largemouth bass, *Micropterus salmoides* and spotted bass, *Micropterus punctulatus* from reservoirs in Alabama and North Carolina. Females of *A. micropteri* differed from those of *A. pimelodi* by having five (vs. one) sickle-shaped (vs. conical) denticles on the second antennae exopod distally and having three setae (ventral, central, dorsal) on the endopod maxillules (vs. two; dorsal and ventral). *Achtheres micropteri* males have three maxillular endopod setae (vs. two) and an armed (vs. corrugated pad) maxilla myxal area. We also add character states associated with the maxillular exopod, maxilliped myxal area, vestigial legs, oviduct, and caudal ramus to taxonomically differentiate *A. micropteri*. Our COI sequences of *A. micropteri* were recovered sister to other *Achtheres* spp.

15. A new species of blood parasite infecting black basses (*Micropterus* spp.) from the Coosa River, Alabama

Micah Brett Warren, Stephen A Bullard

Auburn University, Auburn, AL, USA

Fish blood flukes (Digenea: Chimaerohemecidae; Acipensericolidae; Sanguinicolidae; Elopicolidae; Apocotylidae) are vectored by snails, bivalves, or polychaetes and can kill or debilitate cultured freshwater, marine, and estuarine fishes. Probably many new species remain undescribed in the Southeastern United States, and some could comprise important sportfish pathogens. Freshwater fish blood flukes from North America (Sanguinicolidae) infect trouts (Salmoniformes), basses (Centrarchiformes), minnows (Cypriniformes), and walleye (Perciformes). *Sanguinicola huronis* infects largemouth bass, *Micropterus salmoides* and smallmouth bass, *Micropterus dolomieu* in Wisconsin. However, its morphological description is poor and incomplete, and the single type specimen is damaged making confirmation or comparison impossible. During 2022–2023, the heart/gill of 15 of 381 largemouth bass and 16 of 368 spotted bass, *Micropterus punctulatus* from Neely-Henry Lake (Coosa River) were infected with 13 adults of a new species representing a new genus. Fish blood flukes were fixed in 10% formalin for morphology and preserved in 95% ethanol for DNA extraction and phylogenetic analysis. The new species differs from the other blood flukes by having lateral tegumental spines with a recurved distal tip, a vasa efferentia lacking obvious coalesced efferentia along midline, a triangular ovary, and an oviduct that curves around the terminal portion of the ovary. The 28S phylogeny recovered sequences of the new species as a lineage sister to all sequences representing species of *Sanguinicola*, *Pseudosanguinicola occidentalis*, and related cercarial sequences from Poland and Australia. This is the first fish blood fluke infecting a spotted bass and the second report from largemouth bass. Understanding this group of parasites biodiversity, life cycle, and pathogenicity in black basses is important regarding management of the resource.

16. New taxa illustrate emerging biogeographic patterns of avian schistosomatids (Schistosomatidae: Digenea)

Sara V Brant¹, Pablo Oyarzun-Ruiz²

¹Museum of Southwestern Biology Division of Parasites, University of New Mexico, Albuquerque, New Mexico, USA. ²Laboratorio de Parasitología, Departamento de Microbiología, Facultad de Ciencias Biológicas, Universidad de Concepción, Concepción, Concepción, Chile

Helminths and their migratory hosts provide windows into host–parasite dynamics across spatial and temporal scales, particularly in assessing the concept of host specificity. Avian schistosomatids (Schistosomatidae: Digenea) are blood-dwelling trematodes that use aquatic gastropods as intermediate hosts and birds as definitive hosts. Over the past two decades, research on this group suggests that diversification has been strongly influenced by shifts in gastropod host use, likely facilitated by the broad geographic ranges of migratory avian hosts. Phylogenetic patterns frequently reveal sister lineages distributed along West–East gradients within hemispheres or North–South gradients across the Americas. Recent targeted sampling of underrepresented avian hosts in New Mexico, USA, revealed two novel schistosomatid lineages and previously undocumented host associations. Schistosomatidae sp. 1, collected from *Nycticorax nycticorax* in north-central New Mexico, falls within a clade otherwise represented by cercariae from snails in the family Planorbidae. This lineage is sister to a specimen from Brazil, which in turn is sister to specimens from Kenya, supporting a transhemispheric West–East biogeographic pattern. Schistosomatidae sp. 2, collected from *Recurvirostra americana* in south-central New Mexico, groups with *Riverabilharzia* and is likely sister to *R. ensenadense* described from gulls in Argentina, consistent with a North–South diversification pattern across the Americas. These findings reinforce the importance of integrative sampling across both definitive and intermediate hosts and highlight the role of migratory birds in shaping parasite diversification. More broadly, they emphasize how incomplete life-cycle sampling can obscure host associations and biogeographic structure, leading to underestimates of diversity and misinterpretation of host specificity in this globally distributed parasite lineage.

17. Contrasting genomic signatures of benzimidazole and macrocyclic lactone resistance in *Ancylostoma caninum*

Elise L McKean¹, Young-Jun Choi², Makedonka Mitreva^{2,3}, Damien M O'Halloran¹, John M Hawdon¹

¹The George Washington University, Washington, DC, USA. ²Washington University School of Medicine, St. Louis, MO, USA. ³McDonnell Genome Institute, St. Louis, MO, USA

The development of anthelmintic resistance poses an increasing threat to the treatment and control of parasitic nematode infections. In the dog hookworm *Ancylostoma caninum*, multi-anthelmintic drug-resistant isolates have been identified. While benzimidazole (BZ) resistance is well characterized at the molecular level, driven by canonical mutations in *tbb-iso-1* (β -tubulin isotype 1), including Q134H, F167Y, E198A, and F200Y, the broader genomic context of BZ resistance and the mechanisms underlying macrocyclic lactone (ML) resistance remain poorly understood. To investigate the genomic basis of resistance to these two drug classes, we performed genome-wide F_{ST} -based selection scans on F2 larvae derived from a susceptible (WMD) and resistant (KGR) cross subjected to thiabendazole (TBZ) or ivermectin (IVM) selection in two replicate experiments. Sliding-window F_{ST} and WSTAT statistics were calculated across genomic windows per comparison. TBZ selection produced a highly reproducible genomic signal strongly concordant between replicates. The *tbb-iso-1* locus ranked among the top genome-wide candidates under TBZ selection, with the F167Y resistance allele sweeping to fixation in both replicates, while IVM-selected pools carried this allele at background frequencies consistent with neutral segregation, confirming strong drug specificity. Allele frequency trajectories across the surrounding genomic region are consistent with a hard selective sweep on a shared resistance haplotype. In contrast, IVM selection produced a diffuse, polygenic signal poorly concordant between replicates and spanning multiple genomic regions. This pattern likely reflects the more continuous selective pressure of the larval development assay relative to the binary bottleneck of the egg hatch assay used for TBZ selection and is consistent with a complex multi-locus architecture underlying ML resistance. These results reveal that BZ and ML resistance in *A. caninum* are driven by fundamentally different evolutionary processes, a distinction with practical consequences for how resistance is monitored and managed.

18. Screening and repurposing of antifungal compounds against *Toxoplasma gondii*

Adam Temitope Ajisere¹, Silvia NJ Moreno², Daniel Abugri¹

¹Alabama State University, Montgomery, AL, USA. ²University of Georgia, Athens, GA, USA

Toxoplasma gondii is an obligatory intracellular parasitic protozoan that causes toxoplasmosis. It is responsible for both latent and acute infections in warm-blooded animals. It can be transmitted through contact with cat feces or by ingestion of contaminated meat or water. Individuals with weakened immune systems—such as pregnant women and the elderly are at higher risk. Infection during pregnancy can lead to congenital toxoplasmosis, stillbirth, miscarriage, or neurological damage to the child. *Toxoplasma gondii* has two strains: type I and type II. The latter is associated with chronic disease and forms cysts called bradyzoites. Currently, there are no approved drugs for treating chronically infected strains. The available treatment is a combination therapy of pyrimethamine and sulfadiazine, which can cause side effects in individuals with sulfur intolerance. Other options, such as atovaquone, are less effective against the parasite—particularly the bradyzoite stage. To develop alternative therapies, drug repurposing has emerged as a promising strategy. We hypothesize that antifungal compounds can inhibit *Toxoplasma gondii*. Fungicide library of 140 compounds was screened against *Toxoplasma gondii* at 5 μ M. Out of this number, a total of 13 compounds showed a percentage inhibitions greater than 90% for type I. Next, the effective concentrations (EC_{50s}) of the top 3 compounds (5, 53, and 109) were determined to be 427.1, 452.0, and 854.6 nM, respectively. Also, two of these compounds were effective against the type II strain which are capable of forming bradyzoites. Future studies will evaluate their potency and safety using *in vivo* models and elucidate their mechanism of action.

19. The FDA-approved medication sertraline impairs *Toxoplasma gondii* replication and induces cyst formation in infected host cells

Kathryn Beebe, Lamba O Sangare

Texas A&M University, College Station, TX, USA

Toxoplasma gondii is a common foodborne disease, chronically infecting approximately one-third of the world population. Initial infection via consumption of contaminated food leads to dissemination of the fast-replicating form (tachyzoites) throughout the host, reaching the brain and forming cysts. Individuals with compromised immune systems can suffer from reactivation of these cysts, causing potentially fatal encephalitis. The molecular mechanisms behind cyst formation and reactivation remain poorly understood, limiting the development of treatments against this specific form of *T. gondii*. We discovered that the FDA- approved medication sertraline alters tachyzoite replication and induces cyst formation. Sertraline targets the phosphoproteome of the parasite, targeting both the TgSPARK and TgAMPK pathway. Pathways that are important for parasite replication and cyst formation, as well as metabolic activity, respectively. Our current work is elucidating the roles of TgSPARK and TgAMPK as both independent yet connected kinases and their role in regulating *T. gondii* replication and cyst formation. Our data provide a basis for developing new treatments against *T. gondii* cyst formation and reactivation in infected individuals.

20. Bioactive terpene isolated from *Momordica charantia* plant exhibits potent activity against larval and adult *Ancylostoma* species

Catherine A Jackson¹, Matthew Zincone², Emily Mevers², Andrew N Lowell², John M Hawdon¹

¹George Washington University, Washington, DC, USA. ²Virginia Tech, Blacksburg, VA, USA

Hookworm infections pose a significant health threat in developing countries, particularly affecting vulnerable populations with limited healthcare access. The inevitable emergence of anthelmintic resistance, driven by widespread prophylactic drug administration underscores the urgency for novel treatment approaches. *Momordica charantia*, or bitter melon, is cultured widely in tropical regions where hookworm is endemic and is often used in traditional medicine practice to treat intestinal parasite infections. In previous research, we have used *in vitro* assays with whole aqueous extracts of *M. charantia* to investigate the anthelmintic potential of the plant. Our prior studies have confirmed that whole plant extract is capable of killing adult *Ancylostoma ceylanicum* and can inhibit larval feeding in *Ancylostoma caninum* L3. Following the confirmation of activity, we endeavored to isolate and characterize the specific compound(s) responsible for the lethal effect using high-performance liquid chromatography. Over several rounds of fractionation and larval screening assays, we identified momordicoside L as being a significant contributor to the plant's anthelmintic activity. This isolated product was tested *in vitro* against *A. ceylanicum* adults and *A. caninum* L3. We generated a dose-response curve that demonstrates the lethal activity of momordicoside L against adult hookworm and found that the purified compound can reliably kill *A. ceylanicum* adults. In addition, we optimized an assay using *A. caninum* larvae that serves as a preliminary screening measure, allowing us to generate a significantly more robust characterization of the compound's activity. This screening included an investigation into the efficacy against multi-anthelmintic drug-resistant hookworm, the data from which we believe supports the potential of momordicoside L as a suitable alternative in the treatment of resistant hookworm infections.

22. Extending the lack of evidence for manipulation: No effect of *Parelaphostrongylus* spp. on the behaviour of 2 gastropod intermediate host species

Valeria Pobirohin, Abigail C Finch, Ness Dalling, Jillian T Detwiler

University of Manitoba, Winnipeg, MB, Canada

Many parasites manipulate host behaviour, which can increase the likelihood of transmission. For parasite stages that use several host species, it remains unclear if the parasite affects all host species similarly. *Parelaphostrongylus tenuis* (brainworm) uses at least 25 gastropod intermediate host species and is typically found at low prevalence compared to the prevalence in white-tailed deer definitive hosts. To explain this disparity, the parasite is hypothesized to affect the vertical climbing behaviour of gastropods by increasing their climbing during the morning and evening while white-tailed deer are browsing. Previously, infection in a gastropod species that tends to climb (i.e. arboreal) did not alter climbing. However, the effect of infection on other intermediate host species, including soil-dwelling ones, is unknown. We tested the manipulation hypothesis using 2 ground-dwelling gastropods: *Deroceras laeve* (slug) and *Zonitoides arboreus* (snail). We collected white-tailed deer feces, performed sedimentation to obtain larvae (L1), and exposed and sham-exposed hosts. After the parasites developed to infective L3s (28-31 days), climbing was tested by placing individual gastropods on the bottom of glass cylinders (28 cm × 12.7 cm) and after a 30-minute acclimation period, recording their position (up/down) and height (cm) 4 times every 4 hours. The same individual was tested on 2 days and then all gastropods were dissected to determine infection status. We genetically identified a subset of the L3s to confirm parasite species identification. The climbing position (up/down) and the vertical height were not strongly influenced by infection status in both the slugs and snails. In addition, we found no relationship between position and climbing height according to parasite intensity. Further, we confirmed that gastropods were infected with brainworm and another nematode, musclemworm (*Parelaphostrongylus andersoni*). Despite testing gastropods where the effect of climbing may be more apparent due to their soil-dwelling nature, we find no evidence that *Parelaphostrongylus* species affect gastropod host climbing. White-tailed deer browse on large volumes of leaf litter indicating that even with low prevalence, transmission may occur without parasite manipulation. Alternatively, there may be other ways in which the parasite affects the behaviour of the gastropods that has not yet been tested.

23. Food-web exploiting parasites dominate parasitic load and diversity in Pacific jackknife clams (*Tagelus* spp.)

Chiara G Rizzuti¹, Armand Kuris², Kevin Lafferty^{2,3}, Ryan Hechinger¹

¹Scripps Institution of Oceanography, San Diego, CA, USA. ²UC Santa Barbara, Santa Barbara, CA, USA. ³U.S. Geological Survey, Santa Barbara, CA, USA

Jackknife clams (*Tagelus* species), are one of the most ecologically important animals in California estuaries, yet little is reported about their parasites. Because their parasites may impact the clams and the surrounding food web, we quantified the diversity and abundance of metazoan parasites in 131 clams from 16 sites in two wetlands in California and Baja California: Carpinteria Salt Marsh (CSM) and Estero de Punta Banda (EPB). 100% of the clams were infected by 1–7 parasite species. We detected 12 parasite species overall, with EPB having 66% more than CSM. Correspondingly, the average clam at EPB had approximately double the parasite species richness than that at CSM (2 vs. 4 spp.). Trophically transmitted parasites (mostly trematode metacercariae and “tetracystid” plerocercoids) dominated the combined component communities in terms of abundance (99.9%), biomass (80.9%), and energy flux (85.4%), highlighting the possible importance of jackknife clams as prey for birds and elasmobranchs. A single infection by a trematode parasitic castrator (fellodistomid trematode) composed 16% of the component community biomass and energy flux on EPB mudflats, reflecting their possible importance to the surrounding food web. Biomass and energy-flux loads of individual clams were ~1.6x and ~2x higher on average at EPB than at CSM while exhibiting substantial variability among sites (5–6 fold) within each wetland. At CSM, biomass and energy-flux load first increased with clam size, then substantially decreased in the largest clams. In contrast, EPB biomass and energy-flux

load increased with host body size as theoretically expected, but there were no large-bodied clams. The lack of larger clams at EPB and the decreased parasite load in larger clams at CSM suggest intense behavior modification by trophically transmitted parasites causing elevated predation rates. These findings shed light on parasite diversity and their impact on jackknife clams and their role in estuarine food webs.

24. There and back again: Discovering the complex life cycles of bull shark (*Carcharhinus leucas*) tapeworms

Brooklynn F Minton, Melanie L Langford, Allison Durland-Donahou, Gabriel J Langford

Florida Southern College, Lakeland, FL, USA

Parasites are integral yet often overlooked components of marine ecosystems influencing biodiversity, food web structure, and host population health. Among parasitic taxa, tapeworms (Class Cestoda) are remarkably diverse, with many species exhibiting unique evolutionary relationships with elasmobranchs, the subclass of cartilaginous fishes that includes sharks, rays, and skates. These cestodes display extraordinary morphological adaptations to the spiral valve intestine, reflecting a long coevolutionary history with their hosts. Despite extensive documentation of cestode diversity in elasmobranchs, the complete life cycles of most species remain unresolved. Like other tapeworms, they are believed to pass through multiple intermediate hosts, such as crustaceans and teleost fishes, before reaching maturity in the definitive elasmobranch host. However larval stages are difficult to identify morphologically, and the species host involved in transmission remain largely unknown. This research aims to elucidate the life cycles of elasmobranch cestodes by identifying intermediate hosts and linking larval and adult stages through an integrative approach combining classical parasitology and molecular tools such as PCR and DNA sequencing. Field sampling in the Alafia River and surrounding coastal systems will provide host specimens for morphological and genetic analysis. By reconstructing the developmental pathways of these cestodes, this research will clarify transmission routes, reveal host-specific associations, and improve understanding of how cestodes persist and disperse in marine ecosystems. The results of this ongoing study will be presented at the meeting.

25. Assessing environmental and biotic drivers of parasite assemblages across hosts through time in arid-land streams using museum specimens

Irvin Arroyo-Torres, Thomas F Turner, Lisa N Barrow, Layla Denee, Grace Carmona-Yong, Takuma Shiina, Aridna S Torres, Ethan Thorning, Sara V Brant

The University of New Mexico, Albuquerque, NM, USA

Riparian ecosystems in arid regions display high temporal variability in environmental conditions and community assemblages. Parasite assemblages can reflect shifts in host communities, trophic interactions, and transmission opportunities. This study examines whether biotic or abiotic factors more strongly influence riparian parasite success in the arid Gila River Watershed in the Southwestern United States. From natural history collections, we examined preserved specimens of garter snakes (*Thamnophis* spp.), frogs (*Rana* spp., *Anaxyrus microscaphus*), and fishes (*Agosia chrysogaster*, *Rhinichthys osculus*, *Pantosteus clarkii*, *Catostomus insignis*, *Gambusia affinis*) collected from 1948–2022 for parasites. From these dissections we recorded the parasite assemblages and host size, estimated historical host community composition through records from FishNet2, and integrated modeled historical climate from the PRISM climate group. We then conducted a Sobol sensitivity analysis to determine the proportion of observed variation in infection intensity explained by biotic and abiotic factors. Mean annual temperature appears to be the most important predictor of infection intensity in *Rhabdochona* sp., *Abbreviata* sp., *Haematoloechus* sp. 1, and *Glaridacris* sp. Total annual precipitation was the most important predictor of infection intensity in *Myxobolus* sp., *Contracaecum* sp., *Haematoloechus* sp. 2, and Diplostomidae sp. 3. Infection intensity of *Glaridacris* sp. and Diplostomidae sp. 1 were additionally best predicted by average annual temperature and host size, respectively. Future work will

include more parasite species, fill geographic and temporal gaps in host sampling, conduct more detailed estimations of host community composition, and perform stable isotope analysis of $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$ to evaluate long-term host diet preferences.

26. The striped shore crab (*Pachygrapsus crassipes*) is loaded with diverse parasites that mostly transmit to bird, fish, and shark/ray predators

Sasha L Sypher¹, Armand M Kuris², Kevin D Lafferty^{2,3}, Ryan F Hechinger¹

¹Scripps Institution of Oceanography UCSD, San Diego, CA, USA. ²University of California Santa Barbara, Santa Barbara, CA, USA. ³US Geological Survey, Santa Barbara, CA, USA

The striped shore crab, *Pachygrapsus crassipes*, is an ecosystem engineer and one of the most abundant animals in California and Baja California estuaries, but its parasitism remains poorly understood. Because parasitism may be critical to the crab's ecological role, we quantified parasite load and diversity in 559 crabs from 46 sites in three California/Baja California estuaries. We used abundance, biomass, and energy flux to depict parasite communities and to examine the scaling of total parasite load with host size. Thirteen parasite species were detected overall, spanning various taxa and functional groups: trophically transmitted parasites (trematodes, trypanorhynchs, nematodes), parasitic castrators (bopyrid isopods), typical parasites (gregarines), pathogens (microsporans), and a hyperparasitic parasitoid (putative microsporan). Almost every crab was infected (97% prevalence) by 1–5 parasite species (mean ~2 parasite species). Trophically transmitted taxa dominated aggregated component communities in total individuals (99.9%), biomass (71%), and energy flux (83%), linking crabs to bird, teleost, and elasmobranch predators. Although the large-bodied parasitic castrators were rare (infecting 3% of crabs at EPB and BSQ), they composed a substantial proportion (20%–47%) of the total biomass and energy flux in their component communities. Microsporidian pathogens, likely lethal, infected ~1% of crabs. The putative microsporan parasitoid infected ~1% of microphallid metacercariae. Total parasite biomass and energy-flux loads varied ~2.7-fold among wetlands and exhibited strong within-wetland spatial heterogeneity. Parasite load increased strongly with host size, with abundance rising over 1000-fold and biomass increasing more than 376-fold across the observed size range. However, the increase in parasite load with crab size was weaker for larger crabs, including falling below expectations from parasite scaling theory. This deviation suggests either increased host resistance at larger crab sizes or selective removal of highly infected hosts through predation, consistent with parasite increased trophic transmission. This diverse, variable, yet omnipresent parasite community likely has important effects on the performance of *P. crassipes* and its role in estuarine food webs.

27. Thermal preferences of bivesiculid cercariae

Briana K Zaffiro, Christopher A Blonar, David W Kerstetter, Eloy Martinez

Nova Southeastern University, Davie, FL, USA

Rising global temperatures are likely modulating parasite-host interactions, yet the direction and magnitude of these changes remain uncertain. Previous work on digenean cercariae has largely focused on temperature effects on activity and mortality: in most species, activity increases with temperature to a peak, beyond which it declines sharply; increased activity is typically associated with elevated mortality. However, the underlying metabolic effects of rising temperature on metabolic demands are understudied. The goal of this study was to document the effects of temperature in the aerobic metabolism of bivesiculid cercariae. Each respirometric measurement consisted of 20 bivesiculid cercariae in a modified glass syringe containing Fetig's Medium (Eagles Minimum Essential Medium, 1 mM HEPES, 200 mM L-Glutamin, Antibiotica Mix, 20 mM Glucose Stock, pH: 7.0 at 20°C). Oxygen concentration was measured at five assay temperatures (20°C, 25°C, 30°C, 35°C, and 40°C). Calculated oxygen consumption rates increased with assay temperature, from 3.3 ± 0.96 nL O₂ individual⁻¹min⁻¹ at 20°C to 29.3 ± 8.5 nL O₂ individual⁻¹min⁻¹ at 35°C, and declined to 11.8 ± 2.2 nL O₂ individual⁻¹min⁻¹ at 40°C, indicating a thermal optimum around 35°C. Using the respirometry data

and assuming oxycaloric coefficient for mixed substrates, we estimated temperature-specific energetic demand per cercaria under aerobic conditions, with individuals requiring up to $0.013 \text{ kJ} \cdot \text{mol}^{-1}$ of oxygen per day at 35°C . These estimates allow calculation of both per-parasite potential aerobic energetic demands and the cumulative energetic burden imposed on infected snail hosts under aerobic conditions. As bivesiculid cercariae are released to the environment at later stages, calculated aerobic demands provide a useful estimate of caloric demands by the individual while in the water column in its attempt to be consumed by its next host.

28. Pathogenic infection minimally impacts body condition and immune response in free-ranging Cuban treefrogs, *Osteopilus septentrionalis*, in central Florida, USA

Juliette C Rodrigue^{1,2}, Matthew S Atkinson¹

¹University of Central Florida, Orlando, FL, USA. ²University of Florida, Gainesville, FL, USA

Native wildlife populations have declined as a direct result of pathogenic infections; however, many invasive species appear tolerant of these interactions and may serve as a reservoir on the landscape. The Cuban Treefrog, *Osteopilus septentrionalis*, invaded large portions of the Southeastern United States and could potentially serve as a reservoir for multiple endemic and native pathogens. However, the consequences of infections by these pathogens in Cuban Treefrogs remain poorly understood. Here, we quantified the impact of infection by three different pathogens on the health of Cuban Treefrogs ($n=92$) by analyzing immune response and Fulton's body condition (K). We calculated white blood cell (WBC) percentages and body condition for 92 Cuban Treefrogs collected on the University of Central Florida's Main Campus in Orlando and determined infection status using liver and toe clips for *Batrachochytrium dendrobatidis* (Bd), Ranavirus, and amphibian Perkinsea through established qPCR protocols run as single platforms. Pathogenic infection resulted in little to no impact on the hosts' body condition and WBC percentages, with only Bd showing significantly higher lymphocytes and lower neutrophils ($p=0.009$), in infected individuals. Instead, other factors not related to infection consistently impacted both body condition and leukocyte ratio, including sex, with gravid females exhibiting higher Fulton's K ($p=0.009$) and higher ratios of neutrophils to lymphocytes ($p=0.02$), and the overall highest body condition occurring in August ($p < 0.001$) regardless of host sex. Our study expands upon host consequences for infection in Cuban Treefrogs and adds to the general body of knowledge regarding amphibian hematology and disease ecology.

29. Using historical parasite collection data to reconstruct avian host biology

Sydney E Horan, Janine N Caira, Timothy E Moore, Eric Bae

University of Connecticut, Storrs, CT, USA

Elucidating the life history of a host—especially of understudied or elusive species—poses many logistical challenges. The goal of this study is to determine the extent to which information on the diet and habitat of birds can be derived from their parasites, and specifically their digeneans. The multi-stage life cycle that is both closely tied to specific ecosystems and often involves trophic transmission make these parasites ideal systems for this work. Using the historical Lawrence R. Penner Parasitology Collection, we analyzed a total of 1,013 records of digeneans collected from necropsies of 118 species of North American birds from 1939–1982. Digeneans were identified to a taxonomic level at which their life cycle and associated ecosystem could be determined. We modeled host habitat (e.g., forests, lakes & ponds, marshes, open woodland, shorelines) and diet (e.g. insectivorous, piscivorous) from digenean presence–absence data using multinomial LASSO logistic regression, obtaining an apparent multiclass Brier score of 0.10 (BSS 0.30 vs prevalence baseline) on the training data. These results suggest that parasite presence–absence profiles are highly predictive of host habitat, supporting the idea that trematode communities can serve as effective ecological “fingerprints” of their avian hosts. As a consequence, this approach has the potential to help inform our understanding of hosts with especially elusive life histories. This study is just another example of the value of natural history collections.

30. Fit/fat, or full of parasites? Associations between body fat and helminth infection in an invasive gekkonid

Ryne W Maness, Charles Criscione

Texas A&M University, College Station, TX, USA

While many helminth infections are not lethal, they can reduce host fitness by diverting resources, limiting nutrient availability, or damaging host tissues. For example, activation of immune responses is energetically costly and may shift energy away from growth or reproduction. Additionally, some helminths directly feed on host tissues or digestive material. Infection impacts are often evaluated using body condition indices based on mass and length, but body fat is a more direct measure of energy reserves. Here, we measured body fat using an EchoMRI100-H because it is a noninvasive, quick instrument capable of delivering accurate measurements. This method was validated by a previous study of brown anoles (*Anolis sagrei*) which found that body condition indices showed high variability and weak correlations with body fat, whereas body fat measured using an EchoMRI was strongly correlated with direct fat measurements. Using >600 Mediterranean geckos (*Hemidactylus turcicus*) collected from five locations in southeastern Texas, we tested whether helminth infections were associated with variation in fat reserves. We evaluated the prevalence and abundance of a cestode (*Oochoristica javaensis*), a pentastome (*Raillietiella indica*), and an unidentified oxyurid nematode. For each location, we used generalized linear models and model selection to test parasite effects on body fat separately for males and females. All models included scaled mass index (SMI) to account for size- and age-related variation; female models also included reproductive status to account for elevated fat measurements associated with yolk in fertilized eggs. Effects of infection on fat content were location specific in both sexes, with males showing more frequent/stronger associations with helminth infection. Tapeworms were linked to the largest reductions in body fat, although the strength of these relationships varied among locations. Coinfection effects were generally weak, with one exception in which males co-infected with tapeworms and pentastomes showed evidence of a non-additive association with lower fat reserves. Overall, our findings indicate that helminth parasites have complex, population- and sex-specific associations with host energy reserves in Mediterranean geckos.

31. Assessing the risks of *Sanguinicola* sp. to juvenile spring-run Chinook salmon (*Oncorhynchus tshawytscha*), following Klamath River Dam removal

Hayden A Krause, Sascha L Hallett

Oregon State University, Corvallis, OR, USA

The removal of hydroelectric dams in the Klamath River Basin, completed in Fall 2024, has restored access to critical spawning and rearing habitats for native salmonids, including Spring-run Chinook salmon (*Oncorhynchus tshawytscha*). To support repopulation of these fish above the former dam sites, the Oregon Department of Fish and Wildlife is actively rearing and releasing juvenile Spring-run Chinook salmon from the Klamath Fish Hatchery. However, hatchery-reared juveniles have exhibited signs of *Sanguinicola* sp. infections, including gill hyperplasia, clubbed filaments, and melanization. Historically, the blood fluke *Sanguinicola klamathensis* has been associated with disease outbreaks in rainbow trout at Klamath Fish Hatchery, but infections have not been previously documented in Chinook salmon. To evaluate the risks by *S. klamathensis* to juvenile Spring-run Chinook salmon, we completed an exposure study. *Sanguinicola* sp. adult flukes were first collected from infected hatchery rainbow trout at Klamath Fish Hatchery, for identification. Subsequently, juvenile Spring-run Chinook salmon (2025 cohort) were exposed to one of three concentrations (low, medium, and high dose) of *S. klamathensis* cercariae, alongside an unexposed control group. Following a 30-minute individual exposure, fish were held at the J. L. Fryer Aquatic Animal Health Laboratory for 120 days to monitor disease progression. These results will inform hatchery management and fish releases in Upper Klamath Basin.

32. Intestinal parasites in cats entering local animal shelters in southern Ontario

Alexa Todd, Daniel Lindo, Julia Whale, Jessica Rotolo, John R Barta

University of Guelph, Guelph, ON, Canada

Intestinal parasites pose significant health risks to feline hosts with clinical signs that include diarrhea, abdominal pain, and anemia. Importantly, some parasites of feline hosts are also potential zoonoses. Shelter cats remain an under-studied host population despite having backgrounds that can increase their risk of parasitic infections. This study aimed to identify intestinal parasites present in cats entering local animal shelters to estimate their prevalence and compare these findings with reported data in owned cats and other shelter populations. Fecal samples (n = 57) were collected from four shelters across southern Ontario (Guelph, Kitchener, and Hamilton regions). The samples were analyzed using a modified Cornell-Wisconsin double-centrifugation flotation technique with Sheather's sucrose solution, and slides were examined at 100× total magnification using a compound microscope. Parasites were identified visually in 23 of the 57 samples examined (40.4%) with several cats harboring co-infections. Parasites detected included protists (*Cystoisospora felis*, *C. rivolta*), trematodes (*Paragonimus kellicotti*), cestodes (*Taenia* sp.), and nematodes (*Aelurostrongylus abstrusus*, *Eucoleus* sp., *Ancylostoma* sp., *Toxocara cati*). The observed prevalence exceeded values reported for owned cats and was higher than those reported in other studies that assessed parasite burdens in other shelters located in Ontario. These findings indicate that cats are entering shelters with a high burden of intestinal parasites, highlighting the need for enhanced surveillance, intake screening, and effective treatment protocols in shelter settings.

33. Development of an open-access interactive key for *Lepeophtheirus* (Copepoda: Caligidae) based on original type descriptions and CLSM redescrptions

Felix J Berrios Ortega, James P Bernot

University of Connecticut, Storrs Mansfield, CT, USA

Accurate identification of parasitic copepods is vital for marine ecological research and the management of fish health in aquaculture. The genus *Lepeophtheirus* contains 122 species, including many economically significant ectoparasites; however, identification is challenging due to the large number of species, subtle morphological distinctions, scattered literature, and a lack of identification keys. To address these barriers, we are developing the first interactive identification key for *Lepeophtheirus*, built upon a comprehensive morphological character matrix compiled from original species descriptions and direct specimen examinations. In addition, we are using the matrix to identify correlated characters and defining morphologically related species groups by exploring several different statistical approaches, including discriminant analysis, machine learning, and Bayesian Inference methods. Furthermore, we are redescrbing some of the most poorly known *Lepeophtheirus* species based on type specimens from the Smithsonian National Museum of Natural History. The redescrptions incorporate confocal laser scanning microscopy (CLSM) to detail critical diagnostic traits missing from the original descriptions, thereby ensuring the character matrix is more robust and complete for the interactive key. We are also incorporating taxonomic data from closely related genera, including *Anuretes*, *Pseudanuretes*, *Mappates*, and *Paralebion*, to clarify genus-level distinctions. Diagnostic features are documented using light microscopy, CLSM, and micro-computed tomography (microCT), providing new insights into complex morphological features. Once finalized, the key will be hosted as an open-access resource on the World Register of Marine Species (WoRMS). By combining high-resolution imaging, updated morphological data, and an interactive interface, this project lowers the barrier of entry to copepod taxonomy and establishes a modern, accessible standard for *Lepeophtheirus* identification.

34. Taxonomy and parasitology of some viviparid snails from Alabama and Arkansas

Christine M Smith¹, Stephen S Curran¹, Haley R Dutton¹, John H Brule¹, Daniel Gordillo-González¹, Santiago Escobar-Alfonso¹, Triet N Truong¹, Micah B Warren¹, Stephen A. Bullard^{1,2}

¹Southeastern Cooperative Fish Parasite and Disease Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA. ²Southeastern Cooperative Fish Genetics Laboratory, School of Fisheries, Aquaculture, and Aquatic Sciences, College of Agriculture, Auburn University, Auburn, AL, USA

We investigated the parasites of several populations of mystery snails (*Cipangopaludina* Hannibal, 1912) (Gastropoda: Viviparidae) discovered in 3 localities in north-central Arkansas and 1 location in northern Alabama. We studied snail and parasite morphology, obtained newly generated 18S, 28S, and COI nucleotide sequences from the snails, conducted phylogenetic analyses using the snail sequences, obtained newly generated 18S, 28S, and ITS2 nucleotide sequences for the parasites, and conducted phylogenetic analyses using the parasite sequences. Many if not most GenBank sequences labeled as a species of Viviparidae from North America are nonugens, i.e., they lack a morphological diagnosis or voucher specimen. All sequences from the Alabama viviparids were identical to the GenBank sequences identified as *Cipangopaludina japonica* (E. von Martens, 1861) Hannibal, 1912, and the sequences from the Arkansas viviparids are pending. Parasites were observed alive during dissection and subsequently heat-killed and fixed in formalin or preserved directly in 95% EtOH for morphology and DNA extraction, respectively. From the Alabama viviparids we collected encysted metacercariae of both *Polylekithum ictaluri* (Pearse, 1924) Arnold, 1934 (Digenea: Gorgoderioidea) and *Alloglossidium kenti* Simer, 1929 (Plagiorchioidea). From the Arkansas specimens of *Cipangopaludina* sp. we collected larval (L3) nematodes comprising several species (including *Spiroxys* sp.) (Nematoda: Gnathostomatidae), a cystacanth (Acanthocephala), and encysted metacercariae of *A. kenti* Simer, 1929. No non-native parasite was identified from the study, and we have no reason to think that any of the observed parasites are not native to the area. We think that Enemy Release is an intuitive, quaint idea but largely untested and based upon studies with low sample size, short study duration, low geographic coverage (sampling 1 host population) and low taxonomic resolution.

35. A target capture probe set for copepod phylogenomics

James P Bernot

University of Connecticut, Storrs, CT, USA

Copepods are a class of aquatic crustaceans with about 15,000 described species, though their true diversity is likely much greater. Free-living copepods are typically the dominant component of marine plankton biomass where they form key links in marine food webs and support most fisheries, while parasitic copepods are important pathogens, especially in aquaculture. Despite their ecological and pathogenic importance, phylogenetic relationships among copepods remain poorly resolved, even at the ordinal level. Morphological analyses have been hindered by difficulty establishing homology across highly disparate body plans, which is especially challenging in parasitic lineages. Existing molecular phylogenetic analyses have also not provided robust resolution to the phylogeny because molecular analyses have been limited to a small number of species, less than 200 at most, and a limited suite of genes, with single gene 18S phylogenies predominating. Given the 15,000 extant species of copepod diverged approximately 400 million years ago, it is unlikely a single gene will robustly reconstruct all parts of the copepod tree. Better resolution of the copepod phylogeny awaits high throughput sequencing of multiple genes from many taxa. To address these limitations, I developed a target capture probe set designed for broad applicability across all major groups of copepods. This probe set successfully recovered hundreds of loci from 103 species representing 7 of the 10 recognized orders, providing a scalable framework for phylogenomic reconstruction. In this study, I outline important considerations for probe design in divergent taxa and present preliminary phylogenetic results. These results help clarify relationships among major lineages, reveal several previously unrecognized transitions to parasitism, and provide new insight into the evolution of copepod body plans and host associations.

36. Detection of new *Posthodiplostomum* spp. (Digenea: Diplostomoidea) from the New World

Tyler J Achatz¹, Zoe Von Holten², Makala Fabrizio¹, Theophilus Amporful¹, Stephen Greiman², Kari Waddle³, Nichole Carpenter³, Russell Pfau³, Kristin K Herrmann³, Isabel Blasco-Costa⁴, Sébastien Miche⁴, Sean A Locke⁵, Sydnie F McMahan⁶, Kirsten Jensen⁶, Martin M Montes⁷, Tomas Acuña Gonzalez⁷, Jorge A Barneche⁸, Clara Vercellini⁸, Vasyl V Tkach⁹

¹Middle Georgia State University, Macon, GA, USA. ²Georgia Southern University, Statesboro, GA, USA. ³Tarleton State University, Stephenville, TX, USA. ⁴Muséum d'Histoire Naturelle de Genève, Genève, GE, Switzerland. ⁵University of Puerto Rico–Mayagüez, Mayagüez, PR, Puerto Rico. ⁶University of Kansas, Lawrence, KS, USA. ⁷Universidad Nacional de La Plata, La Plata, BA, Argentina. ⁸Universidad Nacional de La Plata, La Plata, BA, USA. ⁹University of North Dakota, Grand Forks, ND, USA

Posthodiplostomum is a diverse genus of diplostomid trematodes whose metacercariae are responsible for “white grub” disease in freshwater fishes worldwide. The species diversity and evolutionary relationships within the genus remain incompletely resolved. In the present study, we collected adult *Posthodiplostomum* specimens from a variety of avian definitive hosts, as well as immature stages from snails and fishes, in North America. Additionally, metacercariae collected from a fish in Argentina was used to experimentally infect ducks to obtain adults. Morphological study revealed the new material to include four new *Posthodiplostomum* spp.; of which, two represent previously recognized species-level lineages. Additionally, fragments of the large ribosomal subunit (28S) rDNA and cytochrome c oxidase subunit I (cox1) mtDNA gene were sequenced from our samples. Phylogenetic analyses based on 28S demonstrated the new species to be positioned within three of the major clades of the genus. Overall, our study expands current understanding of *Posthodiplostomum* diversity and underscores the importance of integrative approaches combining life-cycle data, molecular phylogenetics, and comparative morphology to resolve systematics and evolutionary patterns in diplostomid trematodes.

37. Identical life cycles in two American alligator trematodes, *Proctocaecum diploporum* and *Proctocaecum coronarium*, from coastal Alabama

Kamila Cajiao-Mora, Stephen S Curran, John H Brule, Daniel Gordillo-González, Haley R Dutton, Micah B Warren, Stephen A Bullard

Auburn University, Auburn, AL, USA

We investigated the life cycle of *Proctocaecum diploporum* and *Proctocaecum coronarium* (Digenea: Cryptogonimidae) obtained during a parasitological survey of the cockscomb hydrobe, *Littoridinops monroensis* (Gastropoda: Cochliopidae), saltmarsh fishes, and the American alligator, *Alligator mississippiensis* (Alligatoridae) within a saltmarsh pond in the Bon Secour Bay (Alabama) and other localities. Cercariae were naturally shed from the cockscomb hydrobe. Fish scales of seven estuarine fish species were infected with two metacercarial cyst size classes, a small (<200µm) and a large (>240µm), suggesting the presence of distinct but closely related sympatric cryptogonimids. Morphological and nucleotide evidence demonstrated that *P. diploporum* (small cyst) and *P. coronarium* (large cyst), previously regarded as taxonomic synonyms, share the same first intermediate host (cockscomb hydrobe), are encysted within the scales of the same fish host species, and mature in the intestine of the same definitive host (American alligator). The taxonomy of these trematodes and that of another similar American alligator trematode, *Caimanicola pavida* (Digenea: Cryptogonimidae), needed reconsideration. Herein, we describe the first complete and naturally occurring life cycle of a reptile-infecting cryptogonimid, provide the first nucleotide data for a species of *Proctocaecum*, taxonomically reassess both *P. diploporum* and *P. coronarium*, and designate a neotype for *P. coronarium*. We consider *C. pavida* as a junior subjective synonym of *P. coronarium*. Phylogenetically related and sympatric trematodes that use the same invertebrate and vertebrate hosts such as these *Proctocaecum* spp. could be a good model to further explore the mechanisms of sympatric speciation and host specificity among trematodes with complex life cycles.

38. Local fauna as a key resource for advancing coccidian taxonomy (and one's career)

John A Hnida

Midwestern University, Glendale, AZ, USA

Since joining Midwestern University (Glendale, AZ) in 2014, I have conducted surveys of the coccidia of round-tailed ground squirrels on the university grounds, Arizona cotton rats and Harris's antelope squirrels in nearby Mesa, AZ, gray-collared chipmunks and golden-mantled ground squirrels in northern AZ, and captive Sonoran Desert tortoises housed by the Phoenix Herpetological Sanctuary. Focusing on local host taxa that had never, or rarely, been surveyed for coccidia resulted in the discovery and description of three new species of eimeriid coccidia and six reports that have expanded the host, and geographic, ranges of ten species of *Eimeria*.

39. GRA70 enhances parasite fitness during IFN γ restriction of *Toxoplasma gondii*

Stephanie Martinez-Beltran, Caroline de Moraes de Siqueira, Jeroen P J Saeij

Department of Pathology, Microbiology and Immunology, School of Veterinary Medicine, University of California Davis, Davis, CA, USA

Toxoplasma gondii is a widespread intracellular protozoan parasite capable of infecting nearly all warm-blooded animals. Following host cell invasion, the parasite establishes a host plasma membrane-derived compartment known as the parasitophorous vacuole (PV), which protects the parasite from cytosolic defenses while serving as the primary interface for host-parasite interactions. Shortly after invasion, *T. gondii* secretes dense granule (GRA) proteins into the PV lumen and parasitophorous vacuole membrane (PVM), where they remodel this compartment to support nutrient acquisition and intracellular replication. In human cells, interferon-gamma (IFN γ) activates a broad antimicrobial program through the upregulation of interferon-stimulated genes (ISGs), including membrane-targeting and ubiquitin-modifying factors that recognize and destabilize pathogen-containing vacuoles. Among these, the E3 ubiquitin ligase Ring Finger Protein 213 (RNF213) and the lipid-modifying enzyme Retinoic Acid Receptor Responder 3 (RARRES3) contribute to parasite restriction in IFN γ -stimulated human cells. However, the mechanisms by which IFN γ destabilizes the PV and how parasite effectors counteract this immune stress to preserve vacuolar integrity remain poorly understood. GRA70, a previously uncharacterized dense granule effector, has emerged as an important mediator of parasite survival under IFN γ stimulation. Here, we tested whether GRA70 promotes parasite survival during IFN γ -mediated restriction by determining whether the IFN γ sensitivity of Δ gra70 parasites depends on the host restriction factors RNF213 or RARRES3. Parasite replication was quantified using parasites-per-vacuole assays, and host cell lysis was measured by lactate dehydrogenase (LDH) release as a proxy for premature parasite egress. We found that Δ gra70 parasites exhibited impaired replication and increased IFN γ -dependent host cell lysis compared to wild-type parasites. Notably, IFN γ -mediated restriction of Δ gra70 parasites persisted in RNF213- and RARRES3-deficient host cells, indicating that the increased sensitivity of Δ gra70 parasites occurs independently of these ISGs. These results suggest that IFN γ may reprogram additional host pathways, potentially lipid metabolic pathways, that alter PVM composition and integrity, compromising parasite survival. Together, these findings identify GRA70 as a determinant of parasite fitness in IFN γ -activated human cells and suggest that parasite effectors help preserve vacuolar integrity during host immune restriction.

40. Impact of the hairworm *Paragordius varius* infection on the fecundity of physid snails

Erik Hatlestad, Ben Hanelt

University of New Mexico, Albuquerque, NM, USA

Physid snails serve as a widespread and commonly available paratenic host for the nematomorph *Paragordius varius* (Nematomorpha: Gordiida), yet the fitness cost of this relationship to the snail host remains poorly

understood. To quantify this cost, we designed an experiment measuring fecundity changes in physid snails infected with *P. varius* by comparing egg mass production and egg counts per mass between infected and uninfected individuals, with outcomes correlated against intensity of infection. This lifecycle has been reliably maintained in laboratory settings at the University of New Mexico and elsewhere. However, at the outset of the experiment in October 2025, the laboratory lifecycle became unstable: physid snails experienced near-total mortality following inoculation with *P. varius*, and dissections revealed substantial larval burden with no cyst formation. These anomalous results prompted a systematic investigation of potential contributing variables, including water source, full-spectrum light exposure duration, inoculation duration, inoculation volume and mechanism, five *P. varius* strains, snail source, and ambient temperature. No single variable was identified as the primary driver of physid mortality. Larval strain trials demonstrated that the larvae retained the capacity to infect and form cysts in other species of water bladder snails and *Biomphalaria* spp., suggesting the disruption was host-specific rather than a general larval dysfunction. Without resolution of the variables affecting cyst formation success, the lifecycle spontaneously returned to normal expected behavior in April 2026. This episode raises novel questions regarding the potential seasonality of *P. varius* infectivity in physid hosts. The originally proposed snail fecundity investigation is now actively underway, and results will be discussed.

41. Short-term ex vivo culture reshapes developmental composition and selectively filters *Plasmodium vivax* haplotypes

Beka Raya R Abagero^{1,2}, Franck Dumetz³, Tirusew Tolosa², Daniel Tesefay², Tassew Shenkutie¹, Biniyam Lukas², Delenesaw Yewhalaw², David Serre³, Eugenia Lo¹

¹Drexel University, Philadelphia, PA, USA. ²Jimma University, Jimma, Oromia, Ethiopia. ³University of Maryland Baltimore, Baltimore, MD, USA

Plasmodium vivax (*Pv*) infections are developmentally asynchronous and often polyclonal, complicating interpretation of bulk parasite transcriptomes. Here, we analyzed paired *in vivo* and short-term *ex vivo* transcriptomes from Ethiopian clinical isolates using stage deconvolution and *PvMSP1* haplotyping. *Ex vivo* maturation modestly increased inferred schizont representation while largely preserving the proportion of trophozoites and gametocytes. After adjustment for parasite stage composition, *in vivo* and *ex vivo* transcriptomes remained globally similar, with no genes significantly differentially expressed, indicating the absence of major culture-induced transcriptional response. In contrast, short-term culture reduced multiplicity of infection, contracted within-host haplotype diversity, and non-randomly depleted specific haplotypes, consistent with a clonal bottleneck. In a subset of low-complexity infections, residual expression patterns were clustered by dominant haplotype, suggesting genotype-associated transcriptional heterogeneity independent of developmental stage. Together, these findings indicate that short-term *ex vivo* culture enriches late asexual stages and selectively filters clones rather than inducing a common transcriptional program. These results shows that *ex vivo* cultures are reliable way to study gene expression, especially for late stages. However, these needs explicitly model developmental composition and infection complexity when interpreting *Pv* transcriptomes from natural infections

42. Distinct HIF-1α signaling pathway in syncytiotrophoblasts mediates the restriction of *Toxoplasma gondii* replication

Dawood A Abbas, Lamba O Sangare

Texas A&M University, College Station, TX, USA

Toxoplasma gondii stabilizes host hypoxia-inducible factor 1α (HIF-1α) to enhance intracellular replication. Although fibroblasts readily support parasite growth, human syncytiotrophoblasts (STBs), the multinucleated cells that form the placental barrier, restrict replication, and the mechanism remains unclear. We

hypothesized that this restriction reflects the parasite's inability to activate HIF signaling in STBs. Using trophoblast stem cell-derived STBs, we found that *T. gondii* does not stabilize HIF-1 α in these cells, in contrast to human foreskin fibroblasts. Failure to induce HIF was associated with reduced tachyzoite replication and increased cyst formation, consistent with a shift toward bradyzoite differentiation. Pharmacologic stabilization of HIF-1 α with CoCl₂ reduced cyst formation, indicating that host HIF activity influences parasite developmental outcome. To explore potential host contributors, we measured mRNA expression of genes linked to parasite-mediated HIF regulation. STBs showed lower transcript levels of prolyl hydroxylase domain protein 2 (PHD2) and activin receptor-like kinases (ALK4/5/7), host factors previously implicated in HIF stabilization pathways during infection. These findings suggest that the transcriptional profile of STBs may limit the parasite's capacity to manipulate HIF-1 α . Together, these data support a model in which impaired HIF-1 α stabilization contributes to placental resistance and influences the replication-to-differentiation transition of *T. gondii*.

43. Temperature-responsive mRNA as a molecular marker of oocyst viability in *Eimeria* spp. using RT-qPCR

Beth Cohen, Parry Kruth, John R Barta

University of Guelph, Guelph, ON, Canada

Assessment of avian coccidiosis viability traditionally relies on in vivo infection models, in which sporulated oocysts are administered to naïve hosts to confirm completion of endogenous development. While effective, this approach is constrained by high costs, labour intensity, and animal welfare concerns. The development of a reliable in vitro proxy for oocyst viability would provide a significant advancement for both research and industry applications. Previous work has identified an mRNA transcript in *Eimeria tenella* that is significantly upregulated during incubation at avian body temperature, consistent with metabolic activation of viable oocysts. This transcript encodes a putative partial translationally controlled tumor protein (TCTP), a protein associated with stress response and cellular proliferation in other eukaryotic systems, though its role in oocyst development and excystation remains uncharacterized. We hypothesize that temperature-induced upregulation of this transcript can serve as a molecular marker of oocyst viability. To expand the applicability of this approach, conserved genomic regions were identified across closely related *Eimeria* species, including *E. acervulina* and *E. maxima*, which represent major burdens to the poultry industry. Primers spanning intronic regions were designed to minimize genomic DNA amplification and accommodate interspecies sequence variation, enabling RT-qPCR-based detection. Species-specific probes and synthetic g-blocks were developed to allow for accurate quantification and potential multiplexing of mixed-species samples. In parallel, an optimized RNA extraction protocol was developed to improve yield and integrity from environmentally resilient oocysts. Together, these methods support the development of a sensitive and reproducible in vitro molecular assay for assessing oocyst viability. This approach has the potential to reduce reliance on animal models while enabling rapid, quantitative evaluation of viability across multiple *Eimeria* species. Additionally, multiplex applications may allow for estimation of species-specific viability within mixed infections, offering valuable tools for both experimental and diagnostic settings.

44. Guanylate-binding proteins balance iNOS/Arg-1 in myeloid cells during *Leishmania major* infection and promote host defense to infection

Lucy Fry, Het Adhvaryu, Hayden Roys, Anne Bowlin, Gopinath Venugopal, Jordan T Bird, Charity Washam, Masahiro Yamamoto, Jörn Coers, Stephanie Byrum, Daniel Voth, Tiffany Weinkopff

University of Arkansas for Medical Sciences, Little Rock, AR, USA

Cutaneous leishmaniasis (CL), caused by *Leishmania major*, is a neglected tropical disease in which parasite persistence within host macrophages drives lesion development and disease severity. While a Th1 response and IFN- γ -mediated activation of macrophages promote parasite control through inducible nitric oxide synthase (iNOS), *Leishmania* can subvert these mechanisms, highlighting the need to define additional host

pathways that restrict intracellular survival. Guanylate-binding proteins (GBPs), a family of IFN-inducible GTPases, are key mediators of cell-autonomous immunity against intracellular pathogens, yet their role during *Leishmania* infection remains unclear. RNASeq analysis revealed that *L. major* infection induces robust up-regulation of multiple GBP family members. Using GBP chromosome 3-deficient (GBPChr3 KO) mice, we found that bone marrow-derived macrophages lacking GBPs exhibit increased intracellular parasite burdens following IFN- γ activation, independent of GBP localization to the parasite. Single-cell RNASeq identified macrophages as the primary GBP-expressing cells during infection in vivo, consistent with their role as the dominant parasite niche. In vivo, GBPChr3 KO mice developed more severe lesions and harbored higher parasite loads. Mechanistically, GBP deficiency skewed macrophages and monocytes toward a parasite-permissive phenotype, characterized by elevated arginase-1 (ARG-1) and reduced iNOS expression. These findings identify GBPs as critical regulators of host resistance to *Leishmania major* by limiting parasite survival within macrophages and maintaining antimicrobial effector balance, revealing a previously underappreciated mechanism controlling intracellular parasite persistence.

45. Comparing the parasite fauna of invasive cane toads and native southern toads within Florida ecosystems

Connor J McCowan, Christina Anaya

Florida Gulf Coast University, Fort Myers, FL, USA

When non-native species enter a new ecosystem, they commonly transport their natural parasites from their native range which may spillover into native species. Establishing baseline checklists of parasites in non-native species is therefore necessary for evaluating spillover. The cane toad, *Rhinella horribilis*, is a common invasive species in Florida's urban ecosystems where it occurs sympatrically with native southern toads, *Anaxyrus terrestris*, a closely related species that may be a competent host to the parasites transported by cane toads. In this study, we are developing a comparative checklist of the helminth parasites infecting the respiratory and digestive systems of cane toads and southern toads from three regions in Florida to establish baseline data for assessing parasite transmission and spillover risk. To achieve this, cane toads were obtained through donations from contractors and homeowners, while southern toads were hand-collected from suburban neighborhoods and adjacent natural areas. In the laboratory, each specimen was weighed, measured and necropsied by removing the lung tissue and digestive tract from the body cavity. Following, each organ was individually separated and lacerated to release the internal contents into a petri dish. Any parasites found were extracted and sorted by genera and morphology. Both host species were infected with 11 parasite species each, including 5 shared taxa across the respiratory and gastrointestinal tracts. Shared parasites include the nematodes *Cosmocercoides* sp. and one unidentified species, the trematodes *Hae-matoloechus* sp. and *Mesocoelium* sp., and a pentastome in the genus *Raillietiella*. *Cosmocercoides* sp. was the most prevalent and abundant parasite in both species and in all regions examined. Infection patterns suggest that some parasites may have originated in Florida native anurans and subsequently infected cane toads, while others may have been introduced by cane toads and then spilled over into native southern toads. Additionally, one parasite likely originated from a separate invasive species and subsequently infected both host species. Our findings reveal the bidirectional exchange of parasites that likely originate from both non-native and native hosts, possibly representing both spillover and spillback. These findings emphasize the critical of host-parasite dynamics and their ecological consequences.

46. A survey of parasites of *Morone saxatilis* (striped bass) in the Hudson River, New York

Delaney F Long¹, Florian B Reyda¹, Jessica E Best²

¹SUNY Oneonta, Oneonta, NY, USA. ²NYS DEC, New Paltz, NY, USA

The Hudson River has been an area of ecological distress, impacting all aspects of the ecosystem. Most affected are the organisms at the top of the food chain, such as striped bass, *Morone saxatilis*, the population

of which has decreased in recent years. Due to this decrease, the New York State Department of Environmental Conservation (NYSDEC) has been conducting collections to monitor the population health of *M. saxatilis* via routine surveys throughout the spring. This project adds a parasitological element to the NYSDEC work with the goal to use parasites as indicators of ecological change. A total of 119 fish were collected via gill net along five different points of the Hudson River during April and May 2026. Specimens were measured, sexed, and dissected, with the intestinal tract examined for parasites with the aid of a stereoscope. Parasites found include the copepod *Ergasilus labracis*, the acanthocephalan *Pomphorhynchus rocci*, the digenetic trematode *Stephanostomum tenue*, the nematode *Philometra rubra*, and the polyopisthocotylean monogenean *Gamacallum macroura*. *Ergasilus labracis* and *G. macroura* were found on the gills, *P. rocci* and *S. tenue* were found in the anterior portion of the intestines, and *P. rubra* was found in the body cavity situating primarily around the vent. The different parasite species present reveal information on host diet and migration patterns, and how to better protect the host population. Notably, the gill-associated parasites *E. labracis* and *G. macroura* may impair osmoregulation and oxygen exchange in heavily infected individuals, representing a potential concern for fish health and fishery stability. Overall parasite prevalence across all sites was high (83-100%) although prevalence of individual species varied. *Ergasilus labracis* occurred at all sites with prevalence ranging from 4-55%, whereas *P. rubra* remained relatively consistent (42-50%). A decreased diversity of parasite species was found in the present study compared to previous parasite surveys of *M. saxatilis* from the Chesapeake Bay. The reduced diversity may reflect shifts in host population size, diet, intermediate host availability, or broader environmental changes. These data provide a baseline on the parasite communities of the Hudson River *M. saxatilis* and their relevance to ecosystem health.

47. The first North American evaluation of parasite diversity and their component community structure in invasive tropical house geckos, *Hemidactylus mabouia*, from Florida

Allison M Bryant¹, Gabriel J Langford², Matthew G Bolek¹

¹Oklahoma State University, Stillwater, OK, USA. ²Florida Southern College, Lakeland, FL, USA

The tropical house gecko is an invasive lizard that was introduced into the United States and Florida in the 1990s. Currently no work exists on the parasites or their component communities in these lizards across North America. To overcome these discrepancies, we collected 35 *Hemidactylus mabouia* individuals in October 2025, from Polk County, Florida Southern College, Florida and examined them for their helminth, pentastome, coccidia, and mite parasites. All parasites were processed according to standard protocols. In addition, the endogenous development of the coccidia was evaluated using histological techniques. The parasitic fauna of *H. mabouia* was composed of seven species, including one mite species (*Geckobia* sp.), one nematode species (*Parapharyngdon* sp.), one cestode species (*Oochorsista javanensis*), one pentastome species (*Raillietiella teagueselfi*), and three species of coccidia (*Eimeria* i.s. *boveroi*, *Isospora hemidactyli*, and *Choleoeimeria* cf. *turcicus*). One hundred percent (35/35) of geckos were infected with mites. Of the endoparasites, the pinworm, *Parapharyngdon* sp., had the highest prevalence (57%) and the pentastome, *R. teagueselfi*, had the highest mean abundance and mean intensity (MA 4.9 ± 6.9 ; range 0-24; MI 8.7 ± 7.1 ; 1-24); whereas of the coccidia species, *E. i.s. boveroi*, had the highest prevalence (46%). Abundance and intensity of parasites tended to increase with body size and there was a significant positive correlation ($r = 0.63$, $P < 0.01$) with lizard snout vent length size and parasite species richness (3.7 ± 1.4 ; 1-6) strongly suggesting that age and/or gape size influenced parasite recruitment. Finally, the endogenous development of the three coccidia species was distinct and genus specific. The endogenous development appears to have a strong phylogenetic signal especially among the *Eimeria*-like coccidia of lizards and will be discussed in more detail.

48. Surveys of *Hypanus sabinus* and *H. say* parasites in the Indian River Lagoon estuary, Florida

Sarah E Sargent¹, David W Kerstetter¹, Joanna Cielocha², Christopher A Blonar¹

¹Nova Southeastern University, Dania Beach, FL, USA. ²Rockhurst University, Kansas City, MO, USA

Despite the wide distribution, abundance, and accessibility of the stingrays *Hypanus sabinus* and *Hypanus say*, the parasite communities of these batoids remain poorly described across much of their ranges, including the Indian River Lagoon (IRL) estuary. Stingrays from the IRL were examined externally and internally for parasites using standard procedures and recovered parasites were identified to the lowest possible taxonomic level. Multivariate techniques were used to explore similarities with published data on parasite communities from congeneric batoid species. Parasite communities of both stingray species were dominated by Cestodes, primarily from the orders Trypanorhyncha and Rhinebothriidea, but also include a diverse community of Monogeneans and Digeneans. Parasite communities of IRL stingrays were broadly consistent with those reported from conspecifics in other study areas; coupled with diet analyses, these data reveal that the IRL supports a diverse host assemblage, implying that this heavily urbanized system remains functionally ecologically robust. Further study of these communities also provides information on natural enemies: as these elasmobranchs typically fill a mesopredatory role, parasites are likely to be the primary agents limiting their populations.

49. Gastrointestinal parasites of gopher tortoises

Michaela S Barnhill¹, Gabriel J Langford¹, Betsie B Rothermel², Rachel Fedders²

¹Florida Southern College, Lakeland, FL, USA. ²Archbold Biological Station, Venus, FL, USA

Archbold Biological Station is located in south-central Florida and contains a well-studied gopher tortoise (*Gopherus polyphemus*) population. Due to a recent upgrade to critically endangered status on the IUCN Red List, it is more important than ever to focus on the general health of this species. In addition, a recently documented case of nonnative pentastome (*Raillietiella orientalis*) infection in the lungs of a seized Galapagos tortoise in a semi-wild south Florida habitat raised concerns of transmission to native tortoises. This study provides a baseline assessment of gopher tortoise intestinal parasites at Archbold Biological Station. Fecal samples were collected from 59 adult tortoises at the field station, then frozen and processed using fecal flotation and sedimentation techniques. Parasite eggs were then identified morphologically using species descriptions and other published literature. While this is an ongoing study, so far 6 species of parasite eggs have been found from the families *Ascaridae*, *Oxyuridae*, and *Strongylidae*. No pentastome eggs have been discovered in the gopher tortoise samples to date. Parasite diversity at Archbold Biological Station is similar to previous studies that were conducted in south Florida and Georgia. Establishing a baseline of parasites is beneficial for evaluating host population health, monitoring spatiotemporal changes in parasite diversity, prevalence, and intensity, and proactively establishing disease management protocols.

50. Endoparasite communities of wading and marsh birds in southern Florida

Alexia Hilber, David Kerstetter, Christopher Blonar

Nova Southeastern University, Fort Lauderdale, FL, USA

The endoparasite community of 24 native Florida wading and marsh bird species from Families Rallidae (rails, coots, and gallinules), Aramidae (Limpkin), Ciconiidae (Wood Stork), Threskiornithidae (Roseate Spoonbill and ibis), and Ardeidae (herons, egrets, and bitterns) are compared. Despite being common among Florida's waterways, limited parasitological information has been documented for these species. Most records in Florida are from over 30 years ago or with minimal sample sizes. As Florida has experienced increased anthropogenic impacts, it is of interest to revisit this community. In addition to cataloging parasites, a comparison of parasitic communities between avian hosts is performed aids in how diet and phylogeny affect infections. Native bird carcasses were received frozen from six wildlife centers across south Florida from 2011 to 2025. We identified 76 genera of parasites from 328 bird carcasses. Overall, 82% of birds examined hosted at least one parasite and 62% exhibited polyparasitism. The ardeids, generalist piscivores, had the highest richness at 47 parasitic genera recovered. The most frequent taxa are *Ascocotyle*, *Contracaecum*, and *Synhimantus*. In contrast, herbivorous rallids were infected by 23 genera,

notably *Notocotylus*, *Capillaria*, and *Polymorphus*. Between the two groups, there is a 13% similarity in parasite community. Wood Storks are infected by seven parasites, major taxa including *Tylodelphys* and *Ascocotyle*. Threskiornithidae hosts 29 parasite taxa, with the most significant being *Patagifer*, *Cyclustera*, and *Parastrigea*. The host families with the greatest similarity in community are the ardeids and Wood Storks (35% similarity) which can be attributed to their overlapping feeding ecology. In contrast, ardeids and rallids are the least similar (13% similarity) among host taxa, chiefly due to differing diet preferences between host groups. These parasite community comparisons can then be used to further describe each wading bird species' role in their environment as well as help explain the interconnectedness of the south Florida wetland environment.

51. Field probiotic treatment reduces fungal pathogen load on wild boreal toads during metamorphosis

Valerie J McKenzie¹, Timothy M Korpita²

¹University of Colorado Boulder, Boulder, CO, USA. ²Fort Lewis College, Durango, CO, USA

Infectious diseases increasingly threaten biodiversity and new approaches to mitigate the effects of harmful pathogens are needed for wildlife conservation. We present results from two field sites involving wild amphibians receiving a probiotic treatment, and one of these occurred during an active infectious disease epizootic event involving the chytrid fungal pathogen *Batrachochytrium dendrobatidis*. We found that Colorado boreal toads (*Anaxyrus boreas*) treated with the probiotic bacteria *Janthinobacterium lividum* were highly sensitive to the developmental timing of treatment, such that only toads treated at the end stages of metamorphosis achieved successful probiotic establishment. As fungal infections increased through the field season, we demonstrated that toads with higher probiotic abundance on their skin had significantly lower fungal infection loads. As fungal pathogens threaten amphibian diversity globally, demonstration of effective pathogen reduction in wild populations, outside of lab conditions, offers insight into the scalability of probiotics for wildlife conservation.

52. *Xenopus laevis* larva as novel model for *Toxoplasma gondii* infection

Daniel A Abugri¹, Homa N Sharma¹, Japhet S Kamasah¹, Alexandra Richard², Mia Smith¹, Jesse Kang¹, Hutton Koehne³, Colin Bodet⁴, Emmanuel Tadjuidje¹

¹Alabama State University, Montgomery, AL, USA. ²Dillard University, New Orleans, LA, USA. ³Life Science Microscopy, Keyence Corporation of America, Atlanta, GA, USA. ⁴Life Science Microscopy, Keyence Corporation of America, Mobile, AL, USA

Toxoplasma gondii (*T. gondii*) is a ubiquitous food and water-borne protozoan with global medical, veterinary, public health, and socioeconomic importance. The parasite is the causative agent of the disease toxoplasmosis. Clinically, the infection could cause encephalitis, ocular disorder, blindness, mental retardation, and stillbirth. Presently, no vaccines or effective drugs are available against the bradyzoite form found as a tissue cyst. Also, the fewer drugs currently administered in the clinic have resistance and toxicity issues. Thus, there is an urgent need to develop new medications against both the bradyzoite and tachyzoite forms of *T. gondii*. There are *in vivo* models available for the study of *T. gondii* transmission and pathogenesis. However, these models are suitable to study aquatic-based infection of the parasite. In this study, we report for the first time the use of *Xenopus laevis* (*X. laevis*) larvae as a rapid, simple, and cheap *in vivo* model for *T. gondii* infection, ocular toxoplasmosis, and cyst formation. Overall, our findings provide unprecedented insight into using the *Xenopus* larva as a simple, cheap, and rapid laboratory *in vivo* model for understanding the biology of water-borne parasites like *T. gondii* in the aquatic system. Also, this discovery showed that infected *X. laevis* larvae could be another intermediate host for transmission of *T. gondii* to water mammals and humans who prey on the infected larvae. The model could also be used to discover drugs for water borne pathogens that affect fish farming among others.

53. Extraocular color discrimination by *Schistosoma mansoni* miracidia

Sonja A Olson, Bailey Stuart, Declan Algreem, Nicolas J Wheeler

University of Wisconsin-Eau Claire, Eau Claire, WI, USA

Schistosoma mansoni miracidia are highly phototactic, using this behavior to select snail microhabitats during host-seeking. However, although photosensation is robust and reproducible, it remains understudied relative to other sensory modalities such as chemosensation. Understanding *S. mansoni* photosensation has implications for infection dynamics and potential control of schistosomiasis, but it is also of basic interest due to the phylogenetic position of *Schistosoma* within the Lophotrochozoa and the apparent absence of obvious photoreceptive organs in any life stage of *Schistosoma* spp., in contrast to other schistosomatids and many other trematodes. Furthermore, technical limitations have restricted prior investigations to white light, leaving wavelength discrimination entirely unexplored despite evidence of spectrally diverse opsins. Here, we show that miracidia discriminate wavelength, preferring blue and green over red, as measured by differential accumulation under narrowband illumination. We further characterize the full repertoire of photobehaviors through feature extraction from tracking data, quantifying the relative contributions of specific behavioral features and comparing them to those displayed during chemokinesis. We also establish the absolute photon flux required to elicit these behaviors. Finally, we examine opsin contributions through phylogenetic analysis, assessment of conserved amino acids implicated in spectral tuning, and integration of single-cell transcriptomics to infer tissue localization in the miracidium. We discuss these findings in light of the broader evolution of photosensory systems across Platyhelminthes and Lophotrochozoa, including the possibility that extraocular color discrimination represents a *Schistosoma*-specific innovation.

54. The impact of eutrophication on parasite diversity in two isolated ponds at the Huston-Brumbaugh Nature Center

Eleanor M Pace, Michael R Zimmermann

University of Mount Union, Alliance, OH, USA

Eutrophication is a growing environmental concern in which nutrient loading into aquatic ecosystems leads to a cascade of events culminating in algal blooms and anoxia, which often decreases biodiversity in the ecosystem. Although the impacts of biodiversity of vertebrate and macroinvertebrate organisms inhabiting these systems have been well-documented, investigation into the impact on parasite diversity is often overlooked. Previous studies have shown that high parasite biodiversity may be an indicator of a healthy ecosystem, but assessing the impact of eutrophication on parasite diversity is rarely documented. The purpose of this study was to determine whether eutrophication impacts parasite diversity across several key vertebrate and invertebrate taxa. This was assessed by collecting organisms from two ponds located at the Huston-Brumbaugh Nature Center of the University of Mount Union in Minerva, Ohio. The East Pond is in an advanced state of eutrophication, and the West Pond is oligotrophic. Parasite diversity was assessed in three major groups of host organisms inhabiting the ponds, (1) Centrarchid fish, the top predators in the ponds, (2) Arthropods, and (3) Gastropods. Macroinvertebrate diversity and parasite diversity in each of the host groups were assessed using the Shannon-Weiner Biodiversity Index and compared between ponds using Hutcheson's t-tests. Macroinvertebrate diversity was significantly greater in the oligotrophic West Pond, however, total parasite diversity was significantly greater in the eutrophic East Pond. This trend was largely driven by the parasite taxa infecting fish, which was greater in the East Pond, while parasite diversity in arthropods was greater in the West Pond. No significant differences were observed in parasite diversity in gastropod hosts between the two sample sites. Contrary to the hypothesis, parasite diversity in the eutrophic system exceeded that of the oligotrophic, indicating that parasite diversity may not always be a good metric for ecosystem health.

55. The perfect storm: Using camera traps, dissections, and precipitation to understand parasite epizootics

Dana M Calhoun¹, Anna M Poslednik¹, Jasmine A Groves^{1,2}, William H Keeley³, Pieter TJ Johnson¹

¹University of Colorado, Boulder, Boulder, CO, USA. ²University of Wisconsin-Madison, Madison, WI, USA.

³City of Boulder's Open Space and Mountain Parks, Boulder, CO, USA

Camera traps are increasingly used to monitor wildlife disease when infections produce visible external signs, yet most parasites, particularly internal helminths, remain largely undetectable despite their potential role in driving epizootic events. In 2022, severe trematode-driven epizootics were documented in amphibians at two freshwater ponds in Boulder, Colorado, providing a rare opportunity to link parasite dynamics with host community activity. At Spring Brook North Pond, infection by *Ribeiroia ondatrae* resulted in severe limb malformations in 70% of metamorphosing northern leopard frogs (*Lithobates pipiens*), a Tier 1 Species of Greatest Conservation Need in Colorado. At Bluestem Connector Pond, larval tiger salamanders (*Ambystoma tigrinum*) harbored an average of 3,125 *Clinostomum marginatum* metacercariae per host, the highest infection reported load, leaving many individuals moribund and unable to swim. To identify drivers of these extreme infection events, we investigated parasite life cycles across multiple hosts from 2022–2025, combining snail dissections to quantify infection prevalence with camera trapping to characterize vertebrate host communities and visitation rates, as trematodes require aquatic snails as first intermediate hosts and vertebrate definitive hosts for transmission. Across both ponds, camera traps recorded 7,508 animals representing 45 species, with peak activity in spring and late summer, and Bluestem Connector Pond supported greater richness (42 species) and abundance (5,325 individuals) than Spring Brook North; the most frequently observed species included wild turkeys (*Meleagris gallopavo merriam*), mallards (*Anas platyrhynchos*), and mule deer (*Odocoileus hemionus*). Time-lag analyses testing whether peaks in definitive host visitation predicted snail infection 4–6 weeks later revealed limited relationship between visitation rates and parasite prevalence; instead, precipitation was negatively correlated with infection, suggesting environmental conditions, rather than host abundance alone, regulate transmission dynamics. Together, these findings highlight the complex, multi-host ecology underlying parasite outbreaks and demonstrate the value of integrating camera trapping with parasitological surveys to provide early warning indicators of disease risk in amphibian populations.

56. Comparative transcriptomic responses to *Schistosoma mansoni* of two *Biomphalaria* taxa from Lake Victoria, Kenya: *B. sudanica* and *B. choanomphala*

Lijun Lu^{1,2}

¹University of New Mexico, Albuquerque, NM, USA. ²Center for Biotechnology Research and Development, Nairobi, Kenya

Background: Lake Victoria harbors two *Biomphalaria* taxa with distinct morphology and susceptibility to *Schistosoma mansoni*. *B. sudanica*, found along shorelines, has large, flat shells and shows less compatibility with infection. In contrast, the deeper-water species *B. choanomphala* has smaller, more angular shells with enlarged body whorls and is highly compatible. Although we are verifying this now through ongoing genome studies, the two snail taxa appear to have very similar genomes but different biological properties, hence their designation as immunotypes. We hypothesize that these differences reflect divergent coevolutionary pressures, with *B. sudanica* mounting stronger anti-trematode responses than *B. choanomphala*. **Methods:** We performed parallel time-series transcriptomic analyses for both species at 12 hours, 2 days, and 5 weeks post-exposure to *S. mansoni*. RNA-seq data were generated from control and exposed groups with multiple biological replicates. Reads from *B. sudanica* were mapped to its reference genome using STAR. Principal component analysis (PCA) was used to assess sample clustering. Differential expression (DE) analysis was conducted using EBSeq, comparing exposed samples to corresponding controls. Genes with fold change ≥ 2 ($\log_2FC \geq 1$) and posterior probability of differential expression > 0.95 were considered significant. For *B. choanomphala*, which lacks a reference genome, reads were mapped to the *B. sudanica* genome using the same analytical pipeline. **Results:** *B. sudanica* samples showed high sequencing and mapping quality,

with unique mapping rates consistently above 85%. PCA revealed clear separation by exposure status and time point. DE analysis identified hundreds of significantly differentially expressed genes at each time point, including many with large expression changes (fold change >8). Transcriptomic analysis of *B. choanomphala* is ongoing. **Conclusions:** These results indicate strong transcriptional responses in *B. sudanica* following *S. mansoni* exposure, consistent with enhanced defense mechanisms. Ongoing comparative analyses with *B. choanomphala* are expected to reveal distinct expression patterns associated with differential susceptibility, providing insight into host–parasite coevolution in these snail taxa. This study was supported by NIH grants P20GM103452 and R37AI101438.

57. The wonderful world of tapeworms

Janine N. Caira

University of Connecticut, Storrs, CT, USA

Join me and my students and colleagues on a journey that spans 40 years (yikes!) discovering the wonders of tapeworms that parasitize sharks and stingrays, and occasionally other vertebrates, across the globe.

58. When clades collide: Genomic admixture in black-legged ticks (*Ixodes scapularis*) from the Great Plains

Kaylee S Herzog¹, Zach Pella², Halie Smith³, Dayna McCormick⁴, Lily Nuss⁵, Amanda Brinkworth², Sujata Chaudhari², Kathryn Duncan⁶, Kellee Sundstrom⁶, Jose E Pietri⁷, Ryan C Smith⁸, Jeff Hamik³, Roberto Cortiñas⁵, Joseph R Fauver²

¹University of New Mexico, Albuquerque, NM, USA. ²University of Nebraska Medical Center, Omaha, NE, USA. ³Nebraska Department of Health and Human Services, Lincoln, NE, USA. ⁴Peru State College, Peru, NE, USA. ⁵University of Nebraska Lincoln, Lincoln, NE, USA. ⁶Oklahoma State University, Stillwater, OK, USA. ⁷Purdue University, West Lafayette, IN, USA. ⁸Iowa State University, Ames, IA, USA

The blacklegged tick or deer tick (*Ixodes scapularis*) is distributed across the Eastern United States and vectors a number of relevant pathogens, including *Borrelia burgdorferi*, the bacteria that causes Lyme disease. Though *I. scapularis* is broadly distributed, Lyme disease transmission does not occur evenly across its range. The majority of human cases are relegated to the Northeast and Upper Midwest, with autochthonous transmission largely absent in southern states despite the presence of the tick vector. This differentiation of *I. scapularis* into a northern and a southern clade is well-recognized, and supported by genotypic and phenotypic differences in addition to differences in *B. burgdorferi* infection rates. The range of *I. scapularis* is expanding westward, with recent colonization of the Great Plains region. Whether the Great Plains will follow patterns of Lyme disease transmission risk similar to northern or southern clade states remains to be determined. To help address this question, we generated the first whole genome sequence (WGS) data from ticks collected in South Dakota, Iowa, Nebraska and Kansas. In a combined population genomic framework including publicly available data from across the range of *I. scapularis* (n=200 individuals), we assessed genomic diversity, population structure, and *B. burgdorferi* infection rates for Great Plains subpopulations. A gradient of genomic admixture between ancestrally northern versus southern clades was inferred for ticks in the Great Plains, with latitude largely driving the proportion of genomic contribution in each subpopulation. Patterns of admixture within Nebraska, however, defy geography. Ticks from the northeastern region of the state had genomes similar to those of northern clade ticks, while ticks from the central eastern region, collected from a nearly identical ecoregion less than 100 miles away, demonstrated equal genomic contributions from northern and southern clades. Furthermore, the northeastern population had rates of *B. burgdorferi* infection of ~50%, while no *B. burgdorferi* infection was detected in ticks from the central eastern population. These results provide further evidence that tick genomics may influence traits associated with *B. burgdorferi* infection status, and thus the potential for Lyme disease transmission.

59. A comparative investigation of tegumental structures and neuromuscular in three cercarial morphotypes from physid snails from Kansas

Sydney F McMahan, Noraida Martínez-Rivera, [Kirsten Jensen](#)

University of Kansas, Lawrence, KS, USA

Cercariae are free-swimming larval stages specialized for transmission from the molluscan intermediate host to the next host. Their morphology is therefore closely associated with locomotory function and host-finding behavior. The goal of this study was to characterize the distribution of tegumental structures, the organization of the musculature, and the interplay between the sensory receptors and nervous system of cercariae representing three morphotypes. Snails of the genus *Physa* were collected between October 2024 and October 2025 from Clinton Lake, Lawrence, Kansas. Snails were isolated and monitored for cercarial shedding. Shed cercariae were identified as *Posthodiplostomum* sp. 23 and *P. centrarchi* (furcocercous cercariae) (Diplostomidae), *Renifer anarium* (xiphidiocercariae) (Reniferidae), and *Lissorchis* cf. *gullaris* (cercarium cercariae) (Lissorchiidae) using a combination of morphological and molecular (partial *28S rDNA* and *COI*) sequence data. Cercariae were examined with scanning electron microscopy (SEM) to characterize the types and arrangement of tegumental structures, and with confocal microscopy (CM) to characterize the neuromusculature. Using SEM, cercariae of the 2 species of *Posthodiplostomum* could be distinguished based on the arrangement of tegumental spines, and sensory receptor type and arrangement on the cercarial body (and tail when present) differed across morphotypes. Staining with phalloidin revealed a conserved organization of muscle fibers in the body wall across morphotypes while differences were seen in the tail musculature in furcocercous cercariae and xiphidiocercariae. Labeling with anti-acetylated α -tubulin and anti- β -tubulin for microtubules associated with cilia, with a DAPI nuclear counterstain, confirmed that the sensory receptors seen with SEM are ciliated. Labeling with anti-synapsin visualized the organization of the cerebral ganglia and nerve commissures and neuronal bodies that innervate the musculature. The number and complexity of nerve commissures and neuronal bodies appeared linked to the number of sensory receptors, whereas cerebral ganglia position and structure were consistent across morphotypes. This study represents the first report of these species from physid snails in Kansas, and the first investigations of these species using SEM and CM. Further investigation is needed into how differences in life history within morphotypes may influence sensory and neuromuscular architecture.

60. An assessment of the host-specificity of *Eimeria* species isolated from four galliform birds (chickens, turkeys, northern bobwhites and chukar partridges)

[Jessica L Rotolo](#), John R Barta

The University of Guelph, Guelph, ON, Canada

Eimeria species are well recognized in the commercial poultry industry for causing coccidiosis, a disease that commonly reduces the health and welfare of intensively reared birds and impacts meat production. These parasites are typically considered to be strictly host-species specific, however, examples of some *Eimeria* spp. capable of infecting multiple galliform hosts have been described previously. Despite the relevance of coccidiosis in commercial poultry production, the number and extent of such cross-infections remain poorly understood. In a series of trials, the host specificity of *Eimeria* spp. isolated from chickens (*Gallus gallus domesticus*), turkeys (*Meleagris gallopavo*), Northern bobwhites (*Colinus virginianus*) and chukar partridges (*Alectoris chukar*) were assessed by attempting to cross-infect coccidia-free chukar partridges, Northern bobwhites and turkeys with single *Eimeria* sp. or mixed species challenges. The success of each cross-infection experiment was assessed using oocyst floatation methods from fecal samples that were collected during the patent period of the coccidia tested. DNA was isolated from the oocysts obtained from the positive samples and, a combination of genus- and species-specific primers were used in a nested PCR to confirm the identity of the *Eimeria* spp. recovered from the feces. Transmission attempts in Northern bobwhites and turkeys with oocysts of *Eimeria chapmani* and *Eimeria hargisi* from chukar partridges were unsuccessful, and none of the *Eimeria* spp. isolated from chickens (i.e., *Eimeria acervulina*, *Eimeria brunetti*, *Eimeria max-*

ima, *Eimeria necatrix* and *Eimeria tenella*) or from Northern bobwhites (i.e., *Eimeria lettyae*) could produce patent infections in the other hosts tested. Few *Eimeria* spp. isolated from turkeys successfully infected multiple hosts, including *Eimeria dispersa* and *E. innocua*, which were shed by both chukar partridges and Northern bobwhites; oocysts of *E. adenoeides* were recovered from chukar partridges only. *Eimeria dispersa* and *E. innocua* were more fecund in turkeys (*E. dispersa*: 95,771; *E. innocua*: 233,026) than in Northern bobwhites (*E. dispersa*: 3,224; *E. innocua*: 3,135) that received equivalent single-species doses. Infections of these euryxenous *Eimeria* spp. could potentially contribute to cases of coccidiosis in captive populations of susceptible gamebirds, particularly when they are located in close proximity to domestic or wild turkeys and reared in high animal densities.

61. Helminth parasites and their snakehead fish hosts in native and invaded ranges

Hsuan-Wien Chen

National Chiayi University, Chiayi, TW, Taiwan

The Striped Snakehead (*Channa striata*), a species widely distributed across Southeast Asia, has successfully established itself in Taiwan over the past three decades. Its large body size, tolerance of polluted waters, parental care behavior, and predatory feeding habits have facilitated its colonization of Taiwan's freshwater ecosystems. Despite its ecological success, the origin and invasion history of *C. striata* in Taiwan, along with its associated parasites and pathogens, remain poorly understood. This study compared the prevalence and diversity of helminth parasites in *C. striata* populations from Taiwan (invaded range) and Thailand (native range) to investigate host–parasite interactions and to elucidate the population genetic structures of both the fish and its parasites. Specimens from both regions were collected and examined for helminth infections. Results revealed that invasive *C. striata* in Taiwan harbored higher parasite prevalence and diversity than native populations in Thailand. The dominant parasites were *Pallisentis* sp. and *Camallanus* sp., which may represent novel species based on morphological and molecular evidence. Parasite spillover was observed among sympatric fishes infected with *Pallisentis* sp., although the worms remained immature. Genetic analyses indicated greater diversity in Thai populations of *C. striata* compared to those in Taiwan, supporting the hypothesis of a single invasion event in Taiwan followed by rapid expansion. Furthermore, the genetic structure of *Pallisentis* sp. exhibited significant differentiation, suggesting host–parasite co-evolution, whereas *Camallanus* sp. showed no clear association with host genetic patterns. This study highlights the complex host–parasite dynamics during the animal invasion, while underscore the importance of parasite diversity, spillover, and co-evolution in invasion biology.

62. Flight fuel and feces: Microbiome dynamics during shorebird stopover

Kate L Sheehan

Frostburg State University, Frostburg, MD, USA

Migratory stopover represents a physiologically dynamic period in which hosts rapidly replenish energetic reserves while experiencing substantial shifts in diet, immune function, and environmental exposure—factors likely to influence host-associated microbial communities with downstream consequences for infection ecology. We examined fecal microbiome assemblages of migratory shorebirds during spring stopover at Delaware Bay, a globally important refueling site where dense mixed-species flocks forage intensively prior to departure for northern breeding grounds. This ecological setting provides a natural framework to evaluate how host physiological condition and species identity structure gut microbial communities during migration. Fecal samples were collected from individually processed Semipalmated Sandpiper (*Calidris pusilla*), Short-billed Dowitcher (*Limnodromus griseus*), and Dunlin (*Calidris alpina*) and paired with morphometric and body condition data. Sampling focused on Semipalmated Sandpipers across multiple stopover weekends spanning a five-week period, providing a temporal series across improving host condition, with complementary samples collected from co-occurring Short-billed Dowitchers and Dunlin during overlapping sampling windows. Mi-

crobial communities were characterized using high-throughput sequencing and evaluated in relation to host condition, sampling period, and species identity. Preliminary analyses indicate that body condition increased predictably throughout stopover, establishing a strong physiological gradient for evaluating microbial community turnover. Early results suggest condition-associated shifts in fecal microbiome composition within Semipalmated Sandpipers, alongside species-level differences among sympatric shorebirds despite broad overlap in stopover habitat and foraging ecology. These findings indicate that host-associated microbial assemblages during migration may be shaped by both rapid physiological change and host-specific biological filtering, providing a foundation for future work linking microbiome restructuring to parasite susceptibility, immune performance, and host health across annual migratory cycles.

63. The anuran tadpole host as a matchmaker for helminth microbiome symbiotic relationships

Matthew G Bolek¹, Alex Bell¹, Ben Hanelt², Sara V Brant², F Agustín Jiménez.³

¹Oklahoma State University, Stillwater, OK, USA. ²University of New Mexico, Albuquerque, NM, USA. ³Southern Illinois University, Carbondale, IL, USA

Tadpoles, the ephemeral, feeding, and non-reproductive larvae of anurans differ significantly in their biology from all other larval and metamorphosed amphibians. Temperate-zone anuran tadpoles are found in streams, ponds, or ephemeral bodies of water, where they feed on suspended and/or epibenthic algae and/or detritus. Tadpole digestive systems are dramatically different from those of predatory adult frogs and go through an ontogenetic niche shift during development. Tadpoles thus are considered vertebrate analogs to larvae of holometabolous insects. This combined ephemeral lifestyle and diet of algae and detritus suggest that tadpoles should not serve as definitive hosts for helminths commonly. Contrary to this expectation, several helminth lineages infect the gastrointestinal tract of larval anurans as definitive hosts worldwide, including amphistome trematodes from two families (Diplodiscidae and Cladorchiidae) and oxyurid nematodes of the family Gyrinicolidae. Examination of these gut-dwelling trematodes reveals the presence of large quantities of algae retained in their ceca that appear bright green and undigested. Because tadpole tissue is transparent over much of the lower body cavity, and trematodes lack cellulolytic enzymes, these observations suggest that ingested algae may be photosynthetically active within the worms, pointing to a more intimate association than simple consumption. Similarly, recent studies on oxyurid nematodes of tadpoles have observed them to be associated with bacteria that grow on their cuticle surface coat. Importantly, visible bacterial clusters are always associated with secretory pores such as the excretory pore, vulva, and/or the cloaca or anus, which suggests an intimate relationship between these nematodes and their bacterial symbionts. We hypothesize that the unique ephemeral lifestyle and the herbivorous/detritivorous diet of tadpoles of anurans may facilitate helminth symbiotic relationships with algae and/or bacteria more commonly than in other vertebrate groups. We discuss the potential of this system as a model for investigating microbiome symbiosis, immune homeostasis, and the coevolution of helminths with their microbial partners and vertebrate hosts.

64. Stretching the truth: Length increase in hairworms post host-emergence

Ben Hanelt, Rachel J Swanteson-Franz

University of New Mexico, Albuquerque, NM, USA

Following completion of development in their terrestrial definitive hosts, hairworms (Nematomorpha: Gordiida) exit the host and enter aquatic environments, where adults mate, deposit eggs, and larvae subsequently encyst in paratenic hosts that return them to the terrestrial food web. Free-living adults may persist for weeks to months. Because most specimens encountered in natural settings are these free-living adults, associated data on definitive host identity and time since host emergence are typically absent. Any morphological changes occurring during this period could therefore compromise the reliability of characters used for species-level identification and phylogenetic inference. Worm length is one such character, notable for its high

variability in natural collections, with reported differences of up to ten-fold between individuals of the same sex. To determine whether post-emergence length change contributes to this variability, we measured mated and unmated male and female *Paragordius varius* from a laboratory population daily from the point of host emergence until death, a period lasting up to 70 days. All 17 individuals increased in length over the measurement period, at a mean rate of 0.026 cm per day (linear mixed-effects model, $p < 0.0001$), representing a mean total gain of 5.7% of initial body length (range 1.3–14.4%). Mated worms grew significantly faster than unmated ones, accumulating length at a rate roughly 40% greater than that of unmated individuals (mating-by-time interaction: +0.009 cm/day, $p = 0.0001$). These results indicate that worm length is a dynamic rather than fixed character in free-living adults and, without reliable emergence time data, should not be used as a diagnostic variable in species descriptions or phylogenetic analyses.

65. Castration comeback: Evidence of post-infection reproduction in a snail host

Kristin K Herrmann

Tarleton State University, Stephenville, TX, USA

Trematode infection often causes castration of first intermediate hosts, eliminating the ability of reproduction in the mollusk host. Castration has been hypothesized as a strategy for extending the life of the host by shifting energy from reproduction to maintenance, thus lengthening the asexually reproductive stage of the trematode. Mollusk host species may evolve adaptations to counteract this negative fitness effect, such as earlier age of reproduction, increase of reproductive output at point of infection prior to castration, or resumption of reproduction post infection. Loss of infection has been demonstrated in several trematode-snail systems. Here, I report observed loss of infection of the trematode, *Stegodexamene anguillae*, in naturally infected snail hosts, *Potamopyrgus antipodarum*. Snails were collected at freshwater field sites in New Zealand in spring and summer of 2008 and maintained in site-collected aerated water. Snails were screened twice for infection with *S. anguillae*. Those not infected were either returned to their original collection site or euthanized. Snails infected with *S. anguillae* were kept in the lab to be used for experimental infections. In spring of 2009, eggs were observed in the container of the previously infected snails. None of the 18 remaining snails shed cercariae, 3 of which were dissected, confirming absence of infection and presence of gametes. Recovery of reproduction in this trematode-snail system adds to previously reported cases and illustrates the ability of some first intermediate host species to recover reproductive ability post-infection.

66. Worms in the Wild West: Parasite community structure and host condition in feral horses

Graham B Goodman¹, Madison Patch², Alex Jones², Sara Weinstein²

¹Utah State University, Price, UT, USA. ²Utah State University, Logan, UT, USA

Feral horses in the western United States receive little veterinary care, making them a rare window into natural host-parasite dynamics in a large North American mammal. We combined fecal flotation with next-generation sequencing (NGS) to characterize parasite communities across six feral herds in Utah and assessed their effects on host body condition. Herds were sampled semiannually ($n = 5$) or monthly ($n = 1$) to detect seasonal and environmental patterns of infection. Community composition and infection intensity varied significantly across space and time, tracking environmental gradients and season. Notably, although deworming campaigns have substantially reduced *Strongylus vulgaris* infection in domestic horses, this highly pathogenic nematode was common across feral herds. Despite harboring diverse parasite communities that included highly pathogenic taxa, parasite burden did not predict host body condition, raising questions about tolerance, compensatory responses, or the sensitivity of body condition as a fitness proxy in wild populations.

67. The role of *Posthodiplostomum* spp. in the maintenance of a subordinate mating strategy of bluegill sunfish (*Lepomis macrochirus*)

Jake Metzger, Michael R Zimmermann

University of Mount Union, Alliance, OH, USA

Bluegill sunfish (*Lepomis macrochirus*) are a common North America sportfish species that exhibit multiple male reproductive morphotypes. Alpha-males invest significantly in the reproductive process through nest-building, courting females, and parental care of the fertilized eggs, while the subordinate β -male morphotype serves as a nest-parasite with no significant parental investment. Despite the far greater reproductive success of α -males, which are responsible for fertilizing 80% of the clutch, the two male morphotypes often exist in relatively equal proportions in natural populations. One hypothesis for this discrepancy between reproductive output and realized abundance in natural populations is that parasites may play a role in limiting the abundance or reproductive success of α -males, thereby enhancing the population sizes of subordinate β -males. This study focused on elucidating the role of one of the most common parasites infecting *L. macrochirus*, the diplostomid parasite *Posthodiplostomum* spp. (white grub). A total of 4,178 *L. macrochirus* was collected from 40 lakes and ponds in Virginia and Ohio to assess the impact of parasite infection on the body condition of the fish hosts. In low abundance, the diplostomid parasite had a significant impact on body condition of the *L. macrochirus* hosts, with the relative weight index consistently around 85. However, when in high abundance (> 900 metacercariae), *Posthodiplostomum* spp. negatively impacted host body condition, dropping the relative weight index score below 80, indicating poor fish health. Furthermore, α -males disproportionately exceeded this parasite threshold with 8.0% of the hosts exceeding, while only 0.4% of β -males reached the excessive infection level. These differences in patterns of diplostomid parasite infection and impact on host body condition may be contributing to the maintenance of a subordinate reproductive morphotype in greater abundance than would be expected based on reproductive output.

68. Prevalence of gastrointestinal parasites in goat (*Capra hircus*) of Malarani Rural Municipality, Arghakhanchi District of Nepal

Naresh Kumar Sah

Himalayan Institute of Agricultural science and Technology, Kirtipur, Bagmati, Nepal

Gastrointestinal parasitic infection in goat is one of the causes of low productivity, morbidity and mortality. This study was conducted to determine the prevalence, intensity of infection and farm management system. Dropping samples were collected from 200 goats from Malarani Rural Municipality, Arghakhanchi, Nepal. Samples were collected in the month of February 2019 and subjected to direct smear, sedimentation and floatation technique for coprological examination. The study revealed that of the 200 samples examined, 132 samples (66%) were found to be positive for gastrointestinal parasites covering seven genera. The most common parasites were found to be *Eimeria* sp. (59.5%), *Strongyle* sp. (33.5%), *Trichuris* sp. (23%), *Haemonchus* sp. (14.5%), *Strongyloides* sp. (13.5%), *Trichostrongylus* sp. (9%) and *Fasciola* sp. (4%). Altogether one genus of protozoan and six genera of helminths parasites were found. There was no significance difference between age wise and sex wise prevalence. Single infection was recorded as the highest (54.54%) followed by double (34.09%), triple (7.57%) and multiple (3.78%).

69. Seroprevalence and risk factors associated with *Toxoplasma gondii* in individuals from Romania with professional exposure

Ana A Ardelean¹, Alexander Olariu², Gheorghe Darabus³, Tudor R Olariu¹

¹Victor Babes University, Timisoara, TM, Romania. ²Menlo School, Atherton, CA, USA. ³Faculty of Veterinary Medicine, Timisoara, TM, Romania

Toxoplasma gondii is estimated to infect one-third of the global population. The aim of the present case-control study was to assess the seroprevalence of *T. gondii* antibodies and the potential risk factors associated with seropositivity in individuals with professional exposure (veterinarians, agricultural workers, veterinary medicine students) compared to healthy blood donors. The study included 218 subjects from Western Romania, divided equally into two groups: 109 individuals with professional exposure which represented the study group and 109 age and gender-matched healthy blood donors, the control group. Serologic testing for the detection of *T. gondii* antibodies was performed using the Pastorex Toxo kit (Bio-Rad, France), a latex particle agglutination assay. This test allows the simultaneous detection of specific IgG and/ or IgM antibodies to *T. gondii*. An epidemiological questionnaire was used to assess potential risk factors for *T. gondii* infection. The overall seroprevalence in the study group was 48.6% (53/109) while in the control group was 43.1% (47/109) ($p=0.42$, OR=1.25, 95%CI 0.73-2.13). Seroprevalence among farmers (63.2%, 24/38) was higher compared to veterinary students (28.6%, 10/35) ($p=0.03$, OR =4.29, 95%CI= 1.6-11.5). Rate of anti-*T. gondii* antibodies was also higher in veterinarians (52.8%, 19/36) compared to veterinary students ($p=0.04$, OR= 2.8, 95%CI 1.04 – 7.47). Seroprevalence tended to increase with age in both study and control groups, reaching 90% in subjects aged 51-60 years from the study group vs. 65% in the control group ($p=0.13$, OR 4.85, 95%CI 0.86 –27.2). Rate of anti-*T. gondii* antibodies tended to be higher in the study group among males, females, inhabitants from both, rural and urban areas compared to the control group. No significant differences in seroprevalence were noted between the study and the control groups regarding pets ownership, consumption of raw meat, smoking status and household owning. In conclusion, while overall seroprevalence did not differ substantially between study and control groups, significant differences were found between occupational categories in the study group. These data suggest that certain types of professional exposure, including agricultural activities or animal-related exposure, may raise the risk of *T. gondii* infection. Additional studies with larger sample sizes are required to support these findings.

70. In silico excretory/secretory protein annotation of *Oochoristica javaensis*, a cyclophyllidean cestode that parasitizes reptiles

Chelsea S Thorn, Charles D Criscione

Texas A&M University, College Station, TX, USA

At the host interface, parasitic helminths release excretory/secretory proteins (ESPs) that mediate immune evasion, nutrient acquisition, and tissue interactions, making ESPs important vaccine candidates, drug targets, and drivers of host–parasite coevolution. Yet, insights into cestode ESPs derive almost exclusively from mammalian-host systems (notably Taeniidae and Hymenolepididae), while ESPs from reptile-infecting cestodes remain uncharacterized, despite the distinct immunological features of reptilian hosts compared to mammals. We present the first comprehensive ESP annotation for a reptile-infecting cestode, the gecko tapeworm *Oochoristica javaensis* (Cyclophyllidae:Linstowiidae). We assembled a chromosome-level reference genome of 88.2 Mb across 9 scaffolds plus the mitochondrial genome (BUSCO completeness 98.7%). MAKER gene prediction incorporating whole-worm RNA-seq, *ab initio* modeling, and protein homology yielded 8,768 genes and a filtered proteome of 8,290 proteins (AED<0.5, primary isoforms; BUSCO 94.1%). Candidate ESPs were identified using a multi-tool pipeline of signal peptide, transmembrane, GPI-anchor, and localization prediction, followed by functional annotation with InterProScan, eggNOG-mapper, and homology searches. We identified 448 candidate ESPs, classified as classical (N=265), GPI-anchored surface (N=39), and non-classical extracellular (N=144). Canonical immunomodulator families included Kunitz-type protease inhibitors (N=16), CAP/SCP/CRISP-family proteins (N=14), cathepsin L/B cysteine proteases (N=14), secreted frizzled-related *Wnt* modulators (N=7), and serpins (N=5). Additional families associated with extracellular vesicles or non-classical secretion included tetraspanins (N=29), heat shock proteins (N=20), annexins (N=11), 14-3-3 proteins (N=7), fatty acid binding proteins (N=5), and peroxiredoxins (N=2). Homology searches against UniProt and WormBase ParaSite supported 95% of predicted ESPs and 92% of the full proteome. Homologs of macrophage migration inhibitory factor, a conserved nematode immunomodulator, were absent, a pattern consistent with other parasitic flatworms. However, antigen B/hydrophobic ligand binding proteins, expanded in Taeniidae and widely studied as cestode immunogens, were represented by only 2 paralogs

in *O. javaensis*. Broader comparative studies, and thus wider taxon sampling, will be needed to determine if the distinct immunological and metabolic profiles of reptilian versus mammalian hosts are associated with the retention or expansion of this or other immunomodulatory families in cestodes. Our current annotation facilitates ongoing studies of life-cycle stage-specific ESP expression and population-level signatures of local adaptation across host populations.

71. Organizational diversity of mitochondrial genomes in adeleorinid and eimeriorinid coccidia (Apicomplexa, Eucoccidiorida)

John R Barta

University of Guelph, Rockwood, ON, Canada

The mitochondrial genomes of coccidia are compact (6-12kb), typically circular-mapping, with greatly reduced gene content compared to other eukaryotic mitochondria, retaining only 3 CDS (cytochrome c oxidase subunits I and III, and cytochrome B) with a varying number of small and large subunit ribosomal DNA fragments ranging from 16 to >180 bp in length scattered in various configurations among the CDS. The comparatively high sequence conservation of the rDNA fragments suggest that they remain 'functional' in some way, despite being fragmented; deep sequencing of small 'non-coding' ncRNA fragments from sporozoites of *Eimeria tenella* have demonstrated that most of these rDNA fragments are transcribed into polyadenylated RNA. At the species level, sequence diversity in any of the CDS regions is generally sufficient for differentiation of closely related coccidia; the adjoining conserved rDNA regions provide useful PCR targets for amplification of these CDS regions for DNA barcoding or whole mitogenome sequencing. For all eimeriid coccidia possessing Stieda bodies in their sporocysts (i.e., *Eimeria*, *Isospora*, *Caryospora*, *Cyclospora* and related genera), the content and organization of the mt genome is well conserved. In contrast, heteroxenous and monoxenous adeleorinid coccidia such as species of *Haemogregarina*, *Hepatozoon*, *Klossiella* and *Klossia* show considerable diversity. The high copy number and PCR-friendly nature of CDS regions make these genetic targets highly suited for species-level diagnostics (e.g. ddPCR or amplicon NGS for mixed parasite infections) and for molecular phylogenetics.

72. Dysregulated lymphatic remodeling promotes immunopathology during non-healing cutaneous leishmaniasis

Lucy Fry¹, Flavia Neto de Jesus², Matheus Batista Carneiro², Hayden Roys¹, Anne K Bowlin¹, Nathan C Peters², Pierre-Yves von der Weid², [Tiffany Weinkopff](#)¹

¹University of Arkansas for Medical Sciences, Little Rock, AR, USA. ²University of Calgary, Calgary, AB, Canada

Cutaneous leishmaniasis (CL) is a vector borne disease that is endemic to tropical and sub-tropical regions of the world disproportionately affecting those of low socioeconomic status. The combined role of the parasite and the host's immune response in determining disease severity has made it challenging to discover new anti-leishmanial treatments. Previous work from our lab has established that the dermal lymphatic network is necessary for wound resolution in a model of healing CL with *Leishmania major* parasites. In CL, lymphatic remodeling allows for accumulated fluid to drain from the lesional site, thereby reducing disease severity. In this report, we present a new mechanism of immunopathology during non-healing CL brought about by *L. amazonensis* infection. We show non-healing CL develops alongside an accumulation of cells and fluid in the skin, resulting in chronic inflammation. Lymphatic remodeling is attenuated during the chronic phase of *L. amazonensis* infection. Moreover, the percentage of proliferating lymphatic endothelial cells (LECs) decreases from 6 to 12 weeks post infection (wpi), leading to a decrease over time in lymphatic vessel (LV) density. To induce lymphangiogenesis, exogenous vascular endothelial growth factor-C (VEGF-C) was administered by adenoviral delivery. VEGF-C increased LV dilation leading to reduced lesion sizes without altering para-

site burdens, arguing targeting the lymphatics can alleviate immunopathology. Taken together, these results show impaired lymphatic function contributes to non-healing disease due to *L. amazonensis* infection and the lymphatics can be targeted to decrease inflammation in the skin during infection.

73. Using metabolomics and lipidomics approaches to deciphering apigeninidin chloride mechanism of action

Miya J Moon, Daniel A Abugri

Alabama State University, Montgomery, AL, USA

Toxoplasma gondii is a globally distributed zoonotic parasite responsible for significant veterinary, medical, and socioeconomic burdens. Current therapeutic options remain limited due to toxicity, cost, and treatment failure and thus underscoring the need for new, safe, and effective anti-parasitic agents. This study employed untargeted metabolomics and lipidomics to decipher the mechanism of action of Apigeninidin chloride (APi) on intracellular *T. gondii* tachyzoites in vitro. *T. gondii* RH-RFP tachyzoites (type I strain) were cultured in hTERT cells and treated with APi (50 μ M), azithromycin (AZ; 50 μ M) as a reference drug, or media control for 24 and 48 hours. Metabolites were extracted using chloroform-methanol (2:1) and analyzed by HPLC coupled to high-resolution mass spectrometry. APi induced distinct, time-dependent alterations in peptides, amino acids, lipids, vitamins, and energy-related metabolites. Notably, APi disrupted peptide biosynthesis, resulting in abnormal accumulation of di-, tri-, and tetrapeptides, and altered several amino acid levels. Similarly, we observed amino acids disruption in AZ which was used as a standard drug. Lipidomic profiling revealed APi-specific increases in key phospholipid and fatty acid species, contrasting with the lipid-reducing effects of AZ. APi also elevated indole-3-lactic acid, lactic acid, and other energy-associated metabolites, suggesting a mechanism distinct from AZ mediated inhibition of TCA-cycle enzymes. Additionally, APi increased D-pantothenic acid production, indicating modulation of coenzyme A-associated pathways. Collectively, these findings demonstrate that APi perturbs protein, lipid, and carbohydrate metabolism in *T. gondii* tachyzoites and provide insight into its potential mechanism of action as a promising anti-toxoplasma compound.

74. Ionophore (A23187) alteration of *Toxoplasma gondii* whole lipidome

Jazmyn R Greggs¹, Homa N Sharma², Daniel A Abugri¹

¹Alabama State University, Montgomery, AL, USA. ²University of Tennessee, Chattanooga, TN, USA

The calcium ionophore A23187 is a weak antibiotic that induces calcium influx in eukaryotic cells. The agent has been used to trigger cellular events in parasites such as *Toxoplasma gondii*. It has been known as a critical factor in various stages of the *T. gondii* lytic cycle, including motility, host cell invasion, and egress. It has also been known that A23187 induces apoptosis activity and reactive oxygen species production (ROS). Though all these are known, the role of A23187 in lipid accumulation remains poorly understood. In the current study, we investigated the effect of A23187 on the whole lipidome of RH-RFP (type 1) *T. gondii* tachyzoites in a concentration-dependent manner. We identified the following lipid classes: Phosphoethanolamine (PE), Phosphocholine (PC), Phosphoserine (PS), Phosphothreonine (PT), and Sphingolipids (SP). The treatment of A23187 on *T. gondii* resulted in essential sphingolipid species formation, such as ceramides, dihydroceramide, and sphingosine, which are associated with the induction of cellular apoptosis and autophagy. Also, the following lipids (fatty acids and derivatives) such as erucamide, 3-oxopalmitic acid, oleamide, and ricinelaidic acid) were also detected in higher levels according to their relative abundances. SPs like N-docosanoylsphinganine and N-palmitoyldihydrosphingomyelin were highly formed in the lower concentration of A23187 but reduced at 4 μ M. PE species such as 1-stearoyl-2-oleoyl-sn-glycero-3-phosphoethanolamine zwitterion, PC, and 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine were also relatively abundant in higher doses of A23187 compared to the control groups. This study demonstrated that A23187 causes important lipid species alterations in *T. gondii*. Our future studies will assess the compound effect on the enzyme pathways associated with this lipid accumulation in vitro and in vivo studies.

75. A systems-level comparative analysis of global gene expression of resistant and susceptible *Biomphalaria glabrata* in response to *Schistosoma mansoni* infection

Abdelmalek Lekired, Coen M Adema, Si-Ming Zhang

Center for Evolutionary and Theoretical Immunology, Department of Biology, University of New Mexico, Albuquerque, NM, USA

The freshwater snail *Biomphalaria glabrata* is an important intermediate host of the trematode parasite *Schistosoma mansoni*, a causative agent of human schistosomiasis. To elucidate mechanisms underlying snail resistance, we leveraged our developed genetic and genomic resources and conducted a systems-level analysis of genome-wide gene expression. We examined two models: (A) homozygous lines iBS90-R (resistant) and iM line-S (susceptible), and (B) recombinant inbred lines (RILs), RIL18-R (resistant) and RIL108-S (susceptible), derived from crossing the model A lines. Resistant lines (R) were fully refractory, whereas susceptible lines (S) were fully susceptible to *S. mansoni*. Transcriptomic profiling of juvenile snails at 6, 24, and 48 hours post-exposure (hpe) to *S. mansoni*, alongside unexposed controls, generated 78 RNA-seq datasets. Distinct constitutive expression profiles were observed across all lines, particularly for immune-related genes including lectins, VlgLs, FREPs, FReDs, antimicrobial factors, and GIMAPs. Following infection, susceptible snails exhibited limited early responses but showed widespread downregulation of immune genes by 48 hpe, while retaining antibacterial activity. In contrast, resistant snails displayed dynamic and complex transcriptional responses indicative of effective immunity. Despite shared defense categories (e.g., AIG-domain proteins, biomphalysins, TEPs, and FREPs), resistant lines showed limited overlap in specific gene responses, with only a few identical genes (including a perlucin-like lectin, a multiple epidermal growth factor protein, and a GIMAP) consistently expressed across time points. Co-expression network analysis identified conserved modules, highlighting the complexity of immune regulation. Notably, resistant lines with different genetic backgrounds but same phenotype appear to employ distinct regulatory strategies, resulting in divergent defense profiles. Together, these findings provide integrative insights into the relationships among genotype, gene expression, and resistance phenotype, advancing understanding of host–parasite interactions in this medically important snail vector.

76. No free rides: Testing migration-parasite hypotheses across a long-distance migrant

Dana M Calhoun¹, Jasmine A Groves^{1,2}, Tyler J Achatz³, John M Kinsella⁴, Stephen E Greiman⁵, Maggie A Young³, Rokeya Ahmed⁵, Vasyl V Tkach⁶, Kara J Cromwell⁷, Pieter TJ Johnson¹

¹University of Colorado, Boulder, Boulder, CO, USA. ²University of Wisconsin- Madison, Madison, WI, USA. ³Middle Georgia State University, Macon, GA, USA. ⁴Helm West Lab, Missoula, MT, USA. ⁵Georgia Southern University, Statesboro, GA, USA. ⁶University of North Dakota, Grand Forks, ND, USA. ⁷University of Montana, Missoula, MT, USA

Migration plays a significant role in shaping host ecology and parasite community dynamics. As hosts move across landscapes, they encounter diverse environments and parasite assemblages, influencing patterns of parasite richness, load, and composition. Several non-mutually exclusive hypotheses have been proposed to explain how migration affects parasite dynamics. *Migratory accumulation*, states that migratory animals should have increased parasite exposure through diverse environments, whereas migratory culling (death of highly infected individuals), *migratory escape* (avoiding exposure by changing route or habitat), and *migratory recovery* (overcoming existing infection during the journey [e.g. clearance of infection]) state that migratory animals should see a decrease in parasite richness and or load. We evaluated these hypotheses using the osprey (*Pandion haliaetus*), a widely distributed, long-distance migratory raptor with a specialized fish-based diet, and distinct evolutionary history that may contribute to its unique helminth communities. We examined gastrointestinal tracts from osprey collected through wildlife rehabilitation centers and museum collections across the United States from 2011-2025 and identified helminths using morphological and molecular approaches. We assessed variation in parasite richness, load, and community composition across migration using statistical modeling. Migration was categorized into two periods: “early” (pre-breeding and

breeding) and “late” (post-breeding and non-breeding) and analyses were conducted across three migratory flyways (Pacific, Interior [Central and Mississippi], and Atlantic). In total, we examined over 300 osprey from 15 U.S. states, of which 95% were infected. Trematodes were the dominant group, followed by nematodes, cestodes, and acanthocephalans. We will further discuss how richness, load, and parasite composition changed across the migratory flyways and “early” and “late” migration time periods. This study provides a large-scale characterization of helminth communities in a specialized migratory raptor and highlights how migration can structure parasite dynamics across time and space.

77. Prevalence of Chagas disease (*Trypanosoma cruzi*) in southeastern Nebraska shelter dogs

Richard E Clopton¹, Sierrah Vermeer¹, Debra T Clopton¹, Jon A Kolman²

¹Peru State College, Peru, NE, USA. ²Tecumseh Animal Clinic, Tecumseh, NE, USA

Trypanosoma cruzi is the etiological agent of Chagas disease, long recognized as an endemic disease of Mexico and Central and South America. Chagas disease has drawn little medical scrutiny in the United States, even though it is a potentially significant human disease with abundant wild and companion animal reservoirs. Human and reservoir cases present clinical syndromes ranging from acute febrility to chronic idiopathic cardiomyopathy. The lack of attention reflects the difficulty in diagnosing chronic cases of Chagas Disease as well as a poor understanding of competent vector species and their distribution. Advances in the understanding of vector competence and distribution, coupled with the development of an effective Lateral Flow Antibody Capture Assays, enable new studies to establish and monitor the distribution of Chagas disease in reservoir and human hosts. No human or animal case has been reported from Nebraska, although reservoir cases have been detected across the southern tier states and as far north as Kansas. As part of a health screening of 80 shelter dogs across 4 shelters, we used the Chagas Detect™ Plus Rapid Test (InBios Inc., Seattle, WA) to test for anti-*Trypanosoma cruzi* IgG antibodies. Overall, 29 of 80 dogs (36%) tested positive for antibodies, including clusters of dogs with no history of travel outside Nebraska. These data demonstrate the expansion of the Chagas Disease risk map across the 40th north parallel.

78. Hunting for *Histomonas*: Surveillance of birds and their nematodes from Pennsylvania, USA

Ryan W Koch¹, Kevin D Niedringhaus¹, Andrew Di Salvo², Justin Brown³, Roderick B Gagne¹

¹University of Pennsylvania, Kennett Square, PA, USA. ²Pennsylvania Game Commission, Harrisburg, PA, USA. ³Pennsylvania State University, University Park, PA, USA

Histomoniasis (blackhead disease) is caused by the protozoan *Histomonas meleagridis* (Order Tritrichomonadida) and can cause high mortality rates in some species of gallinaceous birds. These protozoans can be transmitted by ingesting the eggs of cecal worms (*Heterakis gallinarum*), with the protozoans surviving in *H. gallinarum* eggs in the environment for years. *H. meleagridis* infects the cecum and liver of birds, resulting in necrotic lesions in these organs. Surveillance efforts often focus on birds that are clinically ill or found dead, and as a result, the prevalence of subclinical infections is unknown. Additionally, non-target tissues and samples are typically not tested, such as *Heterakis* nematodes. The primary goal of this study was to conduct surveillance of *H. meleagridis* and related trichomonads in gallinaceous birds throughout Pennsylvania. Tissues were tested for trichomonads via PCR using universal trichomonad primers, targeting the partial 5.8S rRNA region, followed by sequencing of PCR-positive samples. Tissues included liver samples from wild turkeys (*Meleagris gallopavo*) that were clinically ill, or dead and presumed clinically ill. Additionally, because *H. gallinarum* is currently the only known vector for *H. meleagridis*, an effort was made to test multiple species of *Heterakis* worms for *H. meleagridis* to better understand the vectors responsible for transmission. Worms were recovered from subclinical wild turkeys, ruffed grouse (*Bonasa umbellus*), ring-necked pheasants (*Phasianus colchicus*), and domestic chickens (*Gallus gallus domesticus*). Based on our PCR, we detected positive samples in 3% (2/62) of wild turkey livers. In contrast, we detected positive samples in 34%

(25/73) of *Heterakis* spp. nematodes among all birds (5/15 turkeys, 16/51 grouse, 2/5 pheasants, 2/2 chickens). Phylogenetically, turkey and pheasant sequences clustered with *H. meleagridis* from turkeys, whereas grouse and chicken sequences formed distinct clades sister to the *H. meleagridis* clade. Most of the other turkey sequences clustered with *Tritrichomonas* sp. from turkeys, another pathogenic trichomonad. These results suggest that there are multiple species of trichomonads infecting Pennsylvania gallinaceous birds, including potentially undescribed *Histomonas* species. We also report novel nematode-trichomonad associations, suggesting that these pathogens utilize different species of *Heterakis* as vectors for transmission.

79. First record of *Saccularina* sp. in Florida ladyfish (*Elops saurus*)

Emily Durkin, Liza Walker, Kathleen Gillis, Carlos Santamaria, John Ambrosio

University of Tampa, Tampa, FL, USA

This study represents the first record of a parasitic trematode *Saccularina magnacetubula* Louvard et al., 2022 in the Atlantic basin. Using morphological and molecular data, we identified specimens isolated from *Elops saurus* Linnaeus, 1766 in Tampa Bay, Florida as *S. magnacetabula*, a species described from Australian waters. Although previous studies report putative undescribed species of *Saccularina* along the Atlantic coast of North America, we present the first record of *S. magnacetabula*, expanding the species' known range and host associations.

80. When worms wander: Citizen science reveals hairworms on the move in Florida

Christina Anaya

Florida Gulf Coast University, Fort Myers, FL, USA

Citizen science observations are increasingly used in ecological studies but remain underutilized in parasitology. Horsehair worms (phylum Nematomorpha) are often difficult to locate due to their seasonality, small size, and cryptic nature, making them ideal candidates for targeted sampling informed by public observations. Here, we use iNaturalist records to guide field collections and report the first published account of horsehair worms from Florida. Thirty-two worms were collected over two winter sampling periods (January and December 2025) from Timberlane Ravine Park (Tallahassee, FL) using coordinates derived from citizen scientist observations. Worms were primarily recovered from two rainwater puddles located ~15 m from a flowing stream. In January 2025, individuals were found within puddles, consistent with typical aquatic emergence. In contrast, in December 2025, worms were observed actively moving ("questing") across the forest floor among ferns, often oriented toward nearby puddles, either singly or in pairs. A nearby primary stream, characterized by milky runoff, yielded no worms despite targeted searches, whereas a smaller, clear upstream tributary contained three individuals in shallow, pooled margins. Morphological examination identified all specimens as belonging to the genus *Gordius*, based on the presence of a postcloacal crescent, visible calotte, and sexually dimorphic posterior morphology (blunt in females; bilobed in males). Males (mean = 175.1 mm, SD = 34.0, range = 123–262 mm, n = 24) were significantly larger than females (mean = 129.7 mm, SD = 42.8, range = 73.3–229 mm, n = 12; Welch's t-test: $t \approx 3.20$, $df \approx 18$, $p \approx 0.005$; Mann-Whitney U: $U \approx 78$, $p \approx 0.008$), with a large effect size (Cohen's $d \approx 1.22$). Although nematomorphs have been previously recorded from Florida in museum collections, this study provides the first published morphological and ecological description from the region. Notably, the observation of worms actively traversing terrestrial substrates toward aquatic habitats represents a rarely documented behavioral strategy in the phylum. Scanning electron microscopy and molecular analyses are currently underway to confirm species-level identifications and evaluate phylogenetic relationships among specimens.

81. Helminth parasites of two invasive lizards, the green iguana (*Iguana iguana*) and the Chinese water dragon (*Physignathus cocincinus*), in Taiwan

Hsuan-Wien Chen

National Chiayi University, Chiayi City, TW, Taiwan

Southeast Asia, one of the world's most dynamic trading and transportation hubs, provides a distinctive context for studying biological invasions. The region is simultaneously a biodiversity hotspot and highly susceptible to the impacts of invasive species. Alien vertebrates are frequently introduced together with co-invaders such as symbiotic microbes, pathogenic organisms, and parasitic helminths. This study investigates parasitic infections in two invasive reptile species in Taiwan: the green iguana (*Iguana iguana*), native to Latin America, and the Chinese water dragon (*Physignathus cocincinus*), native to Southeast Asia—both introduced primarily through the pet trade. We surveyed wild populations of these lizards to assess parasitic infections and conducted comparative analyses to determine whether parasites were co-introduced with their hosts or shared genera with Taiwan's native parasitic fauna. Results showed that over 90% of wild green iguanas, with one exception, were heavily infected with nematodes, all of which were co-invaded from their native range in the Americas. In contrast, infections in Chinese water dragons were largely composed of parasite genera already established in Taiwan. These contrasting cases highlight how processes such as enemy release, spillover, spillback, and dilution effects shape infection dynamics in invasive species. Our findings underscore the complex ecological consequences of biological invasions and emphasize the need to account for co-invading parasites in invasion biology research.

82. Staring into the void: Finding opportunities for research in non-tenure track roles in academia

Matthew S Atkinson

University of Central Florida, Orlando, FL, USA

While never abundant, tenure-track positions are becoming increasingly rare, with many individuals stuck in the post-doc grind after finishing a Ph.D. Furthermore, the current publish-or-perish model further complicates this dynamic leading to individual level burn-out and the disregard for valuable fields within biology like natural history and taxonomy. However, tenure-track roles are not the only position within academia. Instructor or lecturer positions can provide a fulfilling role within academia and potentially allow you to continue exploring interesting research questions outside of a specific research obligation. Here I present how my current approach to incorporating research throughout my role as a lecturer at the University of Central Florida has allowed me to continue pursuing interesting questions in ecology and natural history. Specifically, I highlight how incorporating high impact practices like research-intensive courses opens the door for continuing research in non-tenure track roles and furthers the accessibility of science to a larger audience that would not be able to participate in research otherwise. Additionally, I explore how incorporating undergraduate mentoring through small student-lead projects can benefit not only the student but also be a benefit to programs that may already be stretched thin. Ultimately, scientific inquiry is not confined to tenure-track roles, and through careful and deliberate course design, instructors and lecturers can still provide a fulfilling role in academia post-graduation and be a benefit for your institution.

83. Introspection as a guiding force in career development

F Agustín Jiménez

Southern Illinois University Carbondale, Carbondale, IL, USA

Professional and personal transitions represent both opportunities and challenges. Some of these transitions are marked by milestones (doctoral graduation), while others are gradual (becoming an expert). Be-

cause of its discrete nature, obtaining a Ph.D. degree is an important milestone that generates a myriad of possible transitions, among which, an academic career is only one. I posit, that introspection must guide the steps taken into a career path, and this should supersede most external expectations that are focused on performance. Introspection allows to identify one's drive and willingness to act as well as identifying one's strengths and weaknesses. This exercise should facilitate identifying one's compatibility with employers' culture and expectations, since at one point these may become a constraint rather than a platform for creative work. Sharing the conclusions of these introspective exercises with significant partners is highly recommended because it increases the chances of the individual to pursue happiness. I will summarize my experiences and describe intrinsic and extrinsic shifts that resulted in my own survival in academia. As far as I can tell, there is no definitive guide to survive the transition from student into a career scientist. This lack of guidance results from the very fundamental notion that we all change, and this change is concurrent with shifts in education, technology, economic opportunity and demographics. Furthermore, our own individual characteristics make us have different levels of risk tolerance and develop a unique set of expectations from both ourselves and our environment. The perception of oneself is always important to continue, adjust or pivot from a career choice.

84. "Infectious" lessons learned from curating problematically preserved parasites

Veronica M. Bueno, Katrina Menard, Bernard Goffinet, Janine N. Caira

University of Connecticut, Storrs Mansfield, CT, USA

As global restrictions pose increased challenges on the collection of vertebrates, historical collections of vertebrate parasites have become invaluable and irreplaceable resources. We are currently in the second of a three-year National Science Foundation funded project to integrate nine collections of metazoan parasites hosted by birds, mammals, amphibians, lizards, snakes, fish, and elasmobranchs into the Lawrence R. Penner Parasitology Collection (LRP) housed at the Biodiversity Research Collections at the University of Connecticut. The collections resulted from fieldwork conducted around the globe between 1940 and 2005 by students and preeminent parasitologists. Parasite taxa include a diversity of arthropods, nematodes, platyhelminths, and other minor groups. Our goals are to stabilize and curate the ~114,000 microscope slides and ~14,000 fluid-preserved vials and jars of specimens, digitize their extensive associated data contained on ~14,000 host necropsy cards and sheets, and provide online access to those data via the LRP database. Undergraduate student assistants worked with us in curatorial, digitization, and databasing tasks. To date, our team has transferred more than 9,000 ethanol-preserved specimens housed in vials sealed with deteriorating silicon stoppers to new vials with archival, screw top lids, and have digitized nearly 12,000 slides and 3,000 associated documents. Together we produced over 13,000 new, high-quality database entries following rigorous data standards (i.e., Darwin Core), enhancing the accessibility and long-term stability of the collection. Challenges we overcame included the fragility of the specimens, overcrowded vials, and samples too large to be removed from intact vials. Specimens mounted on glass slides presented other challenges, such as various degrees of crazing of non-archival mounting medium. In the most extreme cases, specimens were unmounted and remounted in Canada balsam. In less extreme cases we developed a potential alternative method of restoration that shows promise as a permanent solution for stopping further crazing. It saves a considerable amount of time and reduces specimen damage associated with remounting, especially in the cases of more fragile specimens such as tapeworms. We anticipate that some of the solutions we developed for this project may be employed to help remediate issues with wet and dry collections of other metazoan taxa.

85. From hosts to history: A behind-the-scenes look at the diverse holdings of the Museum of Southwestern Biology Division of Parasites

Kaylee S Herzog, Sara V Brant

University of New Mexico, Albuquerque, NM, USA

The Museum of Southwestern Biology Division of Parasites (MSBP) at the University of New Mexico houses the third-largest collection of parasites in North America. Established in 2011, the MSBP is steadily building a reputation as a world-class repository for parasite natural history specimens. The division's diverse holdings include collections with notable strengths in mammal and seabird hosts from the Arctic and Antarctic; small mammal hosts from the desert Southwest, US; raptor hosts from the Midwest, US; and gastropod hosts from around the world. In total, the division holds over 50,000 specimens preserved using a variety of methodologies (e.g., permanent slides for light microscopy, histological sections, formalin- and ethanol-persevered specimens, scanning electron microscopy stubs, and host tissues) encompassing a considerable breadth of parasite diversity. An emphasis on connection to deposited host voucher specimens and tissues highlights is a unique strength of the MSBP collection. Many of its parasite specimens, including those from high-latitude regions, are from hosts that are now considered threatened or endangered. As modern recollection of these hosts and their parasites becomes increasingly challenging or even impossible, access to historical specimens becomes ever more valuable. Here, we will highlight the various collections deposited in the MSBP, demonstrate how to search divisional holdings via the Arctos online collection management information system, and provide guidelines for requesting loans, depositing new specimens, and visiting the collection. Our goals are to encourage the use of MSBP holdings in ongoing research, highlight opportunities for specimen deposition from parasitological project of all varieties, and identify additional avenues for the MSBP to help meet the needs of the growing international community of parasitologists.

86. Developing a baseline of diversity and specificity of avian cestodes in the Atlantic flyway of North America

Anna J Phillips

Department of Invertebrate Zoology, National Museum of Natural History, Smithsonian Institution, Washington, DC, USA

Birds host an incredible 39% of known tapeworm diversity with potentially thousands of species undescribed. These host-parasite relationships have evolved across a diversity of both migratory and non-migratory bird species and shifting landscapes. A better understanding of host associations and infection prevalence will provide insight into how these complex interactions are sustained and function within ecosystems as sentinels of change in an ever-increasingly impacted world and will direct future collecting efforts. A major challenge for studying avian cestodes is accessing host specimens since birds are in decline worldwide due to human activity and climate change. The Smithsonian's National Museum of Natural History has a sizable collection of birds from Audubon's Lights Out participatory science program in Washington, DC collected in 2018, 2023–2025, and spring 2026; birds collected during migrations that died after striking windows. While not ideal for systematic study, morphological vouchers paired with genetic data of the worms from this opportunistic sampling of birds are being used to identify Operational Taxonomic Units (OTUs) and develop baseline data of host associations. Examination of the six most common bird species in the sampling is ongoing. Preliminary results of at least 10 individuals collected in 2024 indicate cestode prevalence was highest in White-throated Sparrow (*Zonotrichia albicollis*; 45%) and Common Yellowthroat (*Geothlypis trichas*; 22%) and was lowest in Ovenbirds (*Seiurus aurocapilla*; 6%). Cestodes were more prevalent in Common Yellowthroat and Gray Catbird (*Dumetella carolinensis*) in the spring 2024 and White-throated Sparrow, Yellow-bellied Sapsucker (*Sphyrapicus varius*), and Song Sparrow (*Melospiza melodia*) in the fall 2024. Genome skimming was performed on the parasites with good results, although none of the worms sequenced could be identified to species-level with genetic data alone. At least five OTUs of cestodes have been detected from birds collected in 2024, all appearing to be members of either Dilepididae or Paruterinidae. Further, this research demonstrates how museums

can work with participatory science programs to access otherwise difficult to obtain vertebrate specimens while facing the biodiversity crisis.

87. Emerging evidence of zoonotic schistosomiasis in humans in Abuja, Nigeria

Solomon M Jacob^{1,2}, Yetunde S Akinbo³, Uwem F Ekpo⁴, Oluwaremilekun G Ajakaye⁵, Zainab Omoruyi⁶, Temitope Agbana⁷, Louise Makau-Barasa⁸, Moses O Aderogba⁸, David Bell⁹, Jean-Carel Diehl⁷, Adedotun A Bayegun⁴, Babatunde I Osanyinbi¹⁰, Juliana Amanyi-Enegela¹¹, Frederick O Akinbo^{12,6}

¹University of Benin, ED, Nigeria. ²Federal Ministry of Health, Abuja, FT, Nigeria. ³Northwestern Memorial Hospital, Chicago, IL, USA. ⁴Federal University of Agriculture, Abeokuta, OG, Nigeria. ⁵Adekunle Ajasin University, Akungba Akoko, OD, Nigeria. ⁶University of Benin, Benin, ED, Nigeria. ⁷Delft University of Technology, Delft, CE, Netherlands. ⁸The Ending Neglected Diseases Fund, New York, NY, USA. ⁹Independent Consultant, Texas, TX, USA. ¹⁰Transfusion Service-Diagnostic Institute, Cleveland, OH, USA. ¹¹Christophel Blinden Mission International, Cambridge, CE, United Kingdom. ¹²Brigham Young University, Provo, UT, USA

Schistosomiasis remains a major public health concern in Nigeria. Although Nigeria has continued to implement the WHO strategies for elimination of the disease using mass drug administration since 2014 with consistent and high therapeutic coverages, impact assessment has continuously shown either stagnant or minimal reduction in prevalence. The aim of this study was to determine the molecular characterization of *Schistosoma* species following several rounds of praziquantel therapy in Abuja, Nigeria. Urine samples were collected from 1,887 participants aged five years and above. Samples were examined for *Schistosoma* eggs using light microscopy. A total of 507 (26.9%) were positive for any form of *Schistosoma* while 91 (4.8%) had atypical *Schistosoma* eggs. DNA was extracted from the pooled ova and analyzed by metagenomic sequencing. DNA sequences confirmed the presence of *S. haematobium* and *S. bovis* in the pooled human urine samples suggesting multiple species or hybrid strains infections. This study provides evidence of possible transmission of multiple schistosome species between humans and animals in Abuja, Nigeria, raising concerns about zoonotic transmission and its implication in schistosomiasis elimination effort in Nigeria. These findings underscore the need for enhanced molecular surveillance to better understand schistosome transmission dynamics in endemic regions.

88. From paralysis to recovery: Molecular drivers of cholinergic recovery in nematodes

Sudhanva S Kashyap, Shruti Gupta, Jacob Wragge

Creighton University, Omaha, NE, USA

Soil-transmitted helminth infections represent a major global public health burden, affecting over one billion people worldwide. Infections caused by *Ascaris*, *Trichuris* (whipworms), and *Ancylostoma* (hookworms) spp. are prevalent in warm, humid regions with limited sanitation, as well as in temperate climates during warmer seasons. These infections disproportionately affect children, leading to severe malnutrition and impaired physical and cognitive development. Control strategies rely heavily on anthelmintic drugs such as albendazole, ivermectin, and nicotinic agonists, including levamisole and pyrantel. However, the emergence of drug resistance poses a significant challenge to sustained disease control. Parasitic nematodes employ complex physiological mechanisms to resist and recover from drug-induced paralysis. Cholinergic tachyphylaxis is a key adaptive mechanism that enables parasites to regain motility during prolonged exposure to the nicotinic anthelmintic levamisole. The ER retention protein NRA-2 plays a central role in regulating the trafficking of assembled nicotinic acetylcholine receptors (nAChRs) to muscle membranes. In the parasitic nematode model *Brugia malayi*, *nra-2* is downregulated in adult females during recovery from levamisole exposure, implicating NRA-2 in the regulation of tachyphylaxis. To further elucidate the molecular basis of this process and identify upstream regulatory pathways, we employ both the parasitic nematode *B. malayi* and the free-living model *C. elegans*. We observe upregulation of DAF-12, a nuclear hormone receptor, in tachyphylactic *Brugia*. Pharmacological activation of DAF-12 with $\Delta 4$ -dafachronic acid significantly enhances

recovery in parasitic worms. Consistent with this, *C. elegans* dauer-constitutive (Daf-c) mutants recover in the presence of levamisole, whereas dauer-defective (Daf-d) mutants fail to recover, supporting a regulatory role for DAF-12 in mediating recovery. Loss of *nra-2* leads to increased surface localization of improperly assembled, ACR-8–containing receptors. ACR-8 is a critical component of levamisole-sensitive acetylcholine receptors (L-AChRs) in parasitic nematodes, though it is not required in *C. elegans*. Mutations in *acr-8* have been associated with levamisole resistance in parasites, underscoring the importance of NRA-2–mediated receptor trafficking. Through gene expression analysis, behavioral assays, and fluorescence imaging, we demonstrate that translocation of ACR-8–containing receptors to the membrane is a key determinant of recovery from drug-induced paralysis.

89. Frequency and treatment implications of isotype-1 β -tubulin mutations in canine hookworms in Florida

Alice C Y Lee¹, Valerie A Lantigua¹, Mahya Dini², Elizabeth Redman², Taylor G Nycum¹, John S Gilleard²

¹University of Florida College of Veterinary Medicine, Gainesville, FL, USA. ²University of Calgary Faculty of Veterinary Medicine, Calgary, AB, Canada

Two mutations in the isotype-1 β -tubulin gene, F167Y and Q134H, have been associated with benzimidazole drug resistance in the canine hookworm *Ancylostoma caninum*. While these single nucleotide polymorphisms (SNPs) are widespread in *A. caninum* from pet dogs across North America based on large-scale studies, the relationship between SNP frequency and treatment outcomes is incompletely understood. In the present study, 8 pet dogs and 23 shelter dogs naturally infected with *A. caninum* were treated with the label dose of fenbendazole, and their resistance status was assessed through fecal egg count reduction (FECR) testing. Eighteen dogs (58%) had an FECR <75%, indicating phenotypic resistance. DNA from *A. caninum* eggs collected pre-treatment were analyzed by deep amplicon sequencing, revealing a high prevalence of the two resistance SNPs: 24/31 dogs (77%) for Q134H and 28/31 (90%) for F167Y. The mean frequency of F167Y was higher in resistant (65.9%) vs. susceptible (14.6%) hookworm isolates ($p < 0.001$), whereas there was no difference for Q134H (17.9% vs. 19.8%, $p = 0.83$). Phenotypic resistance was observed in isolates with F167Y frequencies as low as 44.8%. To evaluate for multiple anthelmintic drug resistance, hookworm eggs from 31 shelter dogs with known pyrantel resistance status – based on FECR – were similarly sequenced. Overall prevalence was 84% for Q134H and 35% for F167Y, while frequency ranged from 0.0-78.6% and 0.0-39.9%, respectively. Mean frequencies were not significantly different for pyrantel-resistant vs. -susceptible isolates, suggesting no clear association between fenbendazole and pyrantel resistance development. Interesting differences were observed in amplicon sequence variants between the fenbendazole- and pyrantel-treated dogs that warrant further investigation.

90. SLO-1 regulation determines emodepside sensitivity in *Caenorhabditis elegans*

Purvash Kadam, Jacob Wragge, Jorrico Suelto, Sudhanva Kashyap

Creighton University, Omaha, NE, USA

Neglected tropical diseases affect millions of people worldwide, particularly in regions with limited access to healthcare, poor sanitation, and low research investment. Among these, lymphatic filariasis is a chronic and debilitating disease caused by filarial parasites, including *Wuchereria bancrofti* and *Brugia* spp., which are transmitted by mosquito vectors. These parasites can persist in the human host for years, producing microfilariae and leading to severe clinical manifestations, including lymphedema, elephantiasis, long-term disability, and social stigma, affecting nearly 120 million individuals globally. Despite its significant global burden, effective treatment options remain limited, particularly for eliminating adult worms. Emodepside, a nematode-specific SLO-1 potassium channel activator, is an emerging macrofilaricidal drug. Because its efficacy depends on functional SLO-1 at the plasma membrane, understanding the regulatory mechanisms controlling SLO-1 expression and trafficking is essential. Misfolded or poorly exported SLO-1 is recognized by the ER-associated degradation (ERAD) pathway and delivered to the proteasome. This process is further

influenced by SKN-1A, an ER-tethered transcription factor, which upregulates proteasome subunits, thereby enhancing SLO-1 removal. Simultaneously, the ER trafficking regulator, NRA-2, determines whether ion channels exit the ER or are retained for quality control, a process that could affect SLO-1 surface expression. Our results show that emodepside exhibits dose and time-dependent effects across genetic backgrounds in the model organism *C. elegans*, with wild-type N2 animals showing the highest sensitivity, *nra-2(ok1731)* mutants showing a reduced response, and *skn-1a(mg570)* mutants showing an intermediate phenotype. These differences indicate that SLO-1 availability is regulated by trafficking and proteostasis pathways that modulate drug response. We therefore hypothesize that ER trafficking and proteasome-mediated degradation constitute an integrated regulatory axis that controls SLO-1 surface expression and emodepside sensitivity. To further test this, we will perform motility assays in *nra-2*; *skn-1a* mutants in the presence of emodepside to assess changes in drug sensitivity and analyze SLO-1 expression and localization in the *nra-2*; *skn-1a* using fluorescence imaging. Finally, we aim to determine how simultaneous perturbation of ER trafficking and proteasome regulation affects SLO-1 function, with the goal of identifying mechanisms to enhance anthelmintic efficacy.

91. Cholinergic tachyphylaxis – convergence or independence of L-AChR machinery and ER protein?

Shruti Gupta, Jacob Wragge, Sudhanva Kashyap

Creighton University, Omaha, NE, USA

Helminth infections affect millions of individuals all over the world. Soil-transmitted helminthiasis (STH) is one of the leading neglected tropical diseases caused by *Ascaris spp.*, *Trichuris spp.*, and *Ancylostoma spp.* These infections are not fatal but have a gradual and long-lasting effect on the infected individual. STH are considered a societal burden as they negatively impact children's education and employment opportunities in adults due to infection-associated morbidities and deformities. Due to the unavailability of vaccines, mass administration of anthelmintic drug is the primary method of treatment. Anthelmintics only kill larvae, and adult worms survive, prolonging the infection. Parasitic nematodes are complex organisms that utilize intrinsic mechanisms to recover from the paralytic effects of anthelmintics. Levamisole, a classical anthelmintic, activates the parasitic L-type nicotinic acetylcholine receptors (L-AChRs), leading to calcium influx followed by muscle paralysis in worms. However, the adult worms recover from levamisole induced paralysis through a phenomenon known as cholinergic tachyphylaxis. Molecular mechanisms contributing to helminth recovery in the presence of levamisole are still unknown. In wild-type *C. elegans*, irreversible paralysis is observed in the presence of levamisole, whereas mutants with defective L-AChR clustering, such as *lev-9* and *lev-10*, exhibit robust recovery at higher levamisole concentrations driven by calcium channel regulation and high intracellular calcium. NRA-2, an endoplasmic reticulum protein, plays a critical role in the regulation of the membrane composition of nAChRs in nematodes. In *Brugia malayi*, downregulation of *nra-2* in the presence of levamisole, drives cholinergic tachyphylaxis and worm recovery. In the free-living model, *C. elegans*, we observe that *nra-2* mutants recover in a concentration-dependent manner in the presence of levamisole, different from previously described recovery in *lev-10* mutants. We observe no change in intracellular calcium levels during recovery, implying that cholinergic tachyphylaxis in *nra-2* mutants is independent of calcium homeostasis. Our study highlights two independent pathways that could mediate cholinergic tachyphylaxis in *C. elegans*. We are currently investigating whether the inhibition of both L-AChR clustering and *nra-2* mediated ER retention are required for parasitic recovery. Identifying potential modulators that could prevent the worm recovery will improve anthelmintic efficacy and reduce the risk of resistance.

92. Towards better schistosomiasis treatment: Pharmacological characterization of the *Sma*-SLO-1 BK channel

Julian V Garcia, Jacob G Wragge, Jorrico D Suelto, Sudhanva S Kashyap

Creighton University, Omaha, NE, USA

Parasitic infections are among the most complex diseases of human and veterinary importance. Often, parasite life cycles involve zoonotic stages that cycle among various animals, including humans. These infections raise many concerns, including the disfigurement experienced by those infected, the chronic nature of infections, social ostracism, the disproportionate impact on children, and the downstream reduction in productivity and economic output. Furthermore, the lack of developed vaccines continues to pose significant challenges for disease management. Most anthelmintic treatments rely on drugs that induce paralysis in parasites. However, given the vast diversity of nematodes and flatworms, no single drug can be expected to be uniformly effective across various parasite species and life stages. Schistosomiasis is a chronic parasitic infection caused by the blood fluke trematode worms of the genus *Schistosoma*. While schistosomiasis is commonly treated with praziquantel, this is only effective against adult stages of *Schistosoma* infections, with larval stages showing reduced efficacy, increasing the risk of resistance. There is an urgent need to characterize new drugs and targets to kill both adults and juveniles effectively. Emodepside is a novel broad-spectrum anthelmintic that effectively kills many nematode species by agonizing the BK channel SLO-1. Furthermore, emodepside has moderate paralyzing activity against *Schistosoma* juveniles *in vitro*. *S. mansoni* SLO-1 channel has conserved emodepside binding pocket and calcium regulatory sites, suggesting it may serve as a promising drug target. In our study, we will use heterologous expression in *Xenopus laevis* oocytes and two-electrode voltage-clamp electrophysiology to characterize *Sma*-SLO-1 as a novel anti-flukicidal target of emodepside.

93. Long-term survival of bivesiculid cercariae in different culture media

Briana K Zaffiro, Christopher A Blonar, David W Kerstetter, Eloy Martinez

Nova Southeastern University, Davie, FL, USA

A limiting factor to investigate cercariae biology lies in their inability to survive outside of their host. In their cercarial stage, digeneans spend time outside of their host, but typically survive at most for up to 24 hours in laboratory conditions. This investigation aims to test various cell culture media and determine if bivesiculid cercariae can be reared in laboratory conditions for longer periods of time. Dark Ceriths (*Cerithium atratum*) were collected along the Intercoastal Waterway near Fort Lauderdale and dissected for Bivesiculid cercariae. Cercariae were reared in Fetig's Medium (Eagles Minimum Essential Medium, 1mM HEPES, 200 mM L-Glutamin, Antibiotica Mix, 20 mM Glucose Stock; pH: 7.0 at 20°C), sucrose-based mitochondrial isolation medium (IMB1: 250 mM Sucrose, 0.5 mM Na₂EDTA, 10 mM Tris, 1 g/L BSA; pH: 7.4 at 30°C), or sucrose-based mitochondrial respiration medium (MiR05: 110 mM Sucrose, 0.5 mM EGTA, 3.0 mM MgCl₂, 80 mM KCl, 60 mM K-lactobionate, 10mM KH₂PO₄, 20 mM Taurine, 20 mM HEPES, 1.0 g/L BSA; pH: 7.1 at 30°C). Cercarial activity was monitored daily and assessed among media using survival curves. Cercarial activity was observed for up to 25 ± 0.03, 8 ± 0.01, and 7 ± 0.02 days in Fetig's Media, Mitochondrial Isolation Media, and Mitochondrial Respiration Media respectively. Decline in survivability and cercarial activity towards the end of each trial was characterized by the degradation or loss of cercarial eyespots, possibly indicating senescence. This study found that cercariae can survive up to 25 days in Fetig's Media. Increased survivability in laboratory settings opens the possibility to studies requiring longer survival such as investigations focusing on cercarial physiology, behavior, or metacercarial encystment.

94. qPCR-based vector-borne pathogen detection in field-collected Maryland ticks and ticks from white-tailed deer carcasses

Cassidy R Landis¹, Madison K Eshleman¹, Maiya S Singer¹, Cassandra A Seminoff¹, Gideon H Schamberger¹, Cory A Petter¹, Kimberly P Tucker², Matthew S Tucker¹

¹Lake Erie College of Osteopathic Medicine, Bradenton, FL, USA. ²Non-affiliated, Bradenton, FL, USA

Multiple tick species exist in Maryland, including the black-legged deer tick (*Ixodes scapularis*), which transmits *Borrelia burgdorferi*, *Anaplasma phagocytophilum*, and *Babesia* species. White-tailed deer (WTD) play a critical role in the *I. scapularis* life cycle, supporting adult tick feeding and reproduction. Increasing incidences of these tick-borne pathogens in humans emphasizes the importance of monitoring transmission. From 2017–2020, >460 ticks were collected at ten Maryland parks by dragging ($n=323$) and from WTD carcasses ($n=140$). Ticks were dissected and identified to species. DNA extracted from ticks was analyzed by a TaqMan qPCR testing algorithm for *I. scapularis* tick actin (M1b), *B. burgdorferi* *sl fliD* (M1b), *A. phagocytophilum* *p44* (M1b), *Babesia microti* *sa1* (M1b), *B. burgdorferi* 16S rRNA (M3) to determine pathogen prevalence. qPCR results found suspected *B. burgdorferi* in 54/458 ticks (*I. scapularis*: 48 positive, 17.7%, *A. americanum*: 6 positive, 3.3%, *D. variabilis*: 0%). *A. phagocytophilum* was detected in 84/463 ticks (*I. scapularis*: 77 positive, 27.1%, *A. americanum*: 7 positive, 4.0%, *D. variabilis*: 0%) with no suspected *B. microti*. Of 54 positive ticks for *B. burgdorferi*, 91% were taken from deer carcasses while 84 positive ticks for *A. phagocytophilum* (90.5%) were taken from deer carcasses. *I. scapularis* and *A. americanum* adult ticks had the highest prevalence of *B. burgdorferi* (*I. scapularis*: 45 positive, 34.62%, *A. americanum*: 4 positive, 21.05%) as compared to nymphs (*I. scapularis*: 3 positive, 9.38%, *A. americanum*: 2 positive, 1.25%), and larvae (*I. scapularis*: 0%, *A. americanum*: 0%). Whereas *I. scapularis* adults had the highest prevalence of *A. phagocytophilum* (74 positive, 55.63%) as compared to nymphs (1 positive, 2.38%) and larvae (2 positive, 1.83%). Fair Hill NRMA had the highest prevalence of *A. phagocytophilum* (11 positive, 73.3%) while Catoctin Mountain Park had the highest prevalence of *B. burgdorferi* (30 positive, 57.7%). The identification of pathogen prevalence per life stage, within specific parks, and by collection method helps provide understanding of the transmission dynamics of tick-borne pathogens. This allows regional park services to keep guests informed about the potential risks of these tick-borne illnesses for improved disease surveillance and mitigation of emerging infections.

95. Molecular surveillance of zoonotic and wildlife apicomplexan parasites in Maryland white-tailed deer sampled at managed hunts

Lauren O Reinfeld, Nicholas R Mill, Cassandra A Seminoff, Jesu L Valencia, Maiya S Singer, Cory A Petter, Cassidy R Landis, Madison K Eshleman, Mckayla G Carr, Kimberly P Tucker, Matthew S Tucker

LECOM Bradenton, Bradenton, FL, USA

White-tailed deer (*Odocoileus virginianus*, WTD) are numerous in the United States and can be reservoirs for vector-borne pathogens. Apicomplexan parasites such as *Plasmodium*, *Babesia*, and *Theileria* spp. are transmitted by mosquitoes and ticks and infect WTD. *Babesia* spp. may infect humans, and the wildlife species *B. odocoilei* is known to cause disease in humans. The aim of this study was to ascertain the prevalence of these parasites in the Maryland WTD population by sampling deer harvested during management programs. From 2017–2020, 246 WTD blood samples were collected from deer carcasses during managed hunts at Maryland state, regional, and national parks. Total samples per park ranged from $n=11$ –74. Giemsa-stained blood smears were analyzed microscopically to quantify parasitemia. Genomic DNA was extracted from WTD blood and used in nested PCR to amplify the 18S rRNA (*Babesia*, *Theileria* spp.) and cytochrome b (*Plasmodium* spp.) genes to identify parasite species. Purified PCR products were subjected to Sanger sequencing. Blood was also tested by TaqMan qPCR for *B. burgdorferi* *s.l. fliD*, *A. phagocytophilum* *p44*, and *Babesia microti* *sa1*. Results demonstrated presence of *B. odocoilei*, *Theileria cervi*, and *Plasmodium* spp. in WTD blood collected from multiple parks within Maryland. The overall average parasitemia detected at the parks ranged from $0.36 \pm 0.24\%$ (Gunpowder Falls State Park—Sweet Air) to $1.82 \pm 1.7\%$ (Seneca Creek State Park). Testing of 215 WTD blood samples by nested PCR found that 54% carried *T. cervi* and 28.4% carried *B.*

odocoilei. Of 200 samples tested for *Plasmodium* spp., 35 (17.5%) were positive, and most were detected at two parks. Testing of 184 WTD blood samples by qPCR found that 62.5% were positive for *A. phagocytophilum*, and none were positive for *Borrelia* or *Babesia* spp. This work demonstrates the spread of parasitic infections in WTD throughout Maryland. *Theileria cervi*, *B. odocoilei*, and *A. phagocytophilum* appear to be naturally carried at moderate to high levels at each park, whereas *Plasmodium* spp. had lower prevalence. Understanding the transmission dynamics of vector-borne pathogens is essential for improving human and wildlife disease surveillance, guiding preventive strategies, and mitigating the impact of emerging infections.

96. Molecular identification of tick-borne pathogens in *Ixodes scapularis* from Monroe County, New York

Gideon H Schamberger, Cassidy R Landis, Matthew S Tucker

Lake Erie College of Osteopathic Medicine, Bradenton, FL, USA

Tick-borne diseases represent an expanding public health concern across the northeastern United States, yet regional surveillance data is limited in many areas. *Ixodes scapularis*, the primary vector of *Anaplasma phagocytophilum*, *Babesia microti*, and *Borrelia burgdorferi*, has been increasingly documented across New York State. *Ixodes* spp. are typically associated with wooded, brushy environments in the eastern United States. In this study, 74 *I. scapularis* ticks were collected from wooded sites in Monroe County, New York, by field dragging. Using a drag cloth method, ticks were collected over multiple visits and stored at -20 °C for further analysis. Ticks were identified to species, life stage, and sex using standard morphological taxonomic keys. Ticks were dissected, and DNA was extracted from all life stages of *I. scapularis* with genomic DNA purification kits. A TaqMan qPCR testing algorithm for *I. scapularis* tick actin, *B. burgdorferi* *sl flid* (M1b), *A. phagocytophilum* *p44* (M1b), *B. microti* *sa1* (M1b), *B. burgdorferi* *16s* rRNA (M3), and *A. phagocytophilum* *msp4* (M3) was used to determine pathogen prevalence. *I. scapularis* larvae (n=15) and adults (n=1) tested negative for all pathogens. Among nymphs (n=58), *B. burgdorferi* was detected in 21.4%, representing 16.2% of all ticks tested. *A. phagocytophilum* was detected in 1.4% of samples. *B. microti* was absent across all life stages. Notably, environmental conditions during sampling, including elevated temperatures, increased rainfall, and humidity, may have influenced tick activity. These findings confirm the presence of clinically relevant tick-borne pathogens in Monroe County, New York, and are consistent with historically reported prevalence levels of these pathogens. These data highlight the need for continued surveillance to better characterize the distribution and prevalence of tick-borne pathogens in the region.

97. Predator-parasite interactions and their implications for aquaculture health and sustainability

Molly E Deinhart, Kate L Sheehan

Frostburg State University, Frostburg, MD, USA

Baitfish aquaculture plays a critical role in supporting recreational fisheries and regional economies, particularly in Arkansas, which produces over two-thirds of the nation's baitfish. Fish yields depend on healthy fish stocks and safe working conditions; however, parasite transmission remains a threat to both. While producers attempt to control pond environments, frequent interactions with non-cultured wildlife make biocontrol difficult. These interactions create pathways for pathogens to move between aquatic and terrestrial hosts. Predators' role in pathogenic cycling within baitfish systems remains unclear, limiting the efficacy of disease mitigation strategies and jeopardizing fish and human health. Here, we evaluate avian and mammalian predators' roles on disease in Golden Shiner (*Notemigonus crysoleucas*) aquaculture systems. We collected and necropsied Common Grackles (*Quiscalus quiscula*) and several mammalian predators from baitfish farms. We identified parasites and quantified abundance, intensity, and diversity (H' and $1/D$). We evaluated patterns of taxonomic groups and species using chi-square, ANOVA, and PERMANOVA analyses. Parasites occurred in avian and mammalian predators; however, the communities' risk to aquaculture yields and worker safety differed. Grackles contained parasites and evidence of fish consumption, but all parasites we recovered have strictly terrestrial life cycles and pose no risk to baitfish or humans through their interaction in aqua-

culture systems. Thus, grackles' role is limited to that of a nuisance species, consuming fish and damaging infrastructure. In contrast, mammalian predators harbored greater parasite species diversity, including species with partially aquatic life cycles known to use fish as intermediate hosts. Semi-aquatic species frequently move between aquatic and terrestrial habitats, positioning them as key vectors that connect ecological systems and sustain parasite life cycles. Several mammalian parasites encountered pose zoonotic risks, highlighting hazards for aquaculture workers through exposure to contaminated water, soil, or wildlife waste. We clarify mammalian predators' role as important contributors to parasite transmission in baitfish aquaculture and verify the limited role of avian species such as grackles. However, traditional waterbird predators have not been explicitly evaluated in these systems. Our research can be a basis for the development of more targeted management strategies that reduce disease transmission, improve fish health, and protect human safety in aquaculture systems.

98. Comparison of COI and 28S metabarcoding to traditional parasitological methods for four snake taxa

Alexandria Nelson¹, Abigail Finch¹, Victor Shr¹, Jeff Beane², Michael Cove², Kenzie Pereira¹, Skylar Hopkins¹

¹North Carolina State University, Raleigh, NC, USA. ²North Carolina Museum of Natural Sciences, Raleigh, NC, USA

Environmental DNA and metabarcoding have become increasingly popular methods to indirectly detect parasites within an environment or within a host. However, helminth metabarcoding can be taxonomically restricted due to limitations in existing parasite sequence data, particularly for understudied hosts like snakes. Previous studies have designed protocols for identifying general diet items or specific parasites (e.g., *Railietiella orientalis*) from snake feces, but to our knowledge, no metabarcoding protocols exist that have been designed to broadly detect a variety of parasite taxa from snakes. We developed and tested a pipeline that can use non-invasive swabs of captured animals to provide high resolution snapshots of internal parasite communities. First, we developed the pipeline using salvaged roadkill specimens of Timber rattlesnakes (*Crotalus horridus*, species of special concern in North Carolina), Northern pine snakes (*Pituophis melanoleucus*, threatened in North Carolina), and watersnakes (*Nerodia* spp., least concern in North Carolina). We dissected these individuals to identify internal helminth and pentastome parasites and then barcoded these parasites with Sanger sequencing. During our dissections, we documented 14 unique parasites, which we used to build a reference DNA library: 2 Acanthocephala, 1 Cestoda, 8 Nematoda, 1 Pentastomida, and 4 Trematoda. We then tested the pipeline on hosts where full dissections were not possible: a longitudinal study of live *Nerodia* spp. caught in Wake County, North Carolina (cloacal swabs) and an invasive Burmese python (*Python bivittatus*) removal program that preserved cloacal swabs or feces. Swab preservation medium and snake species had significant impacts on post-extraction DNA concentrations, and DNA concentrations did impact the number COI ASVs (Amplicon Sequence Variants) that made it through the metabarcoding pipeline. We successfully detected parasite COI and 28S DNA across the three dissected host species, live *Nerodia* spp., and python samples. The parasite taxa detected from our metabarcoding pipeline aligned well with the parasite taxa detected from two traditional parasitological methods: dissections and fecal floats. We will discuss cases when parasites were detected with metabarcoding and not parasitological methods and vice versa, along with pros and cons of the metabarcoding workflow.

99. Marine ectoparasite communities on batoid hosts

Lydia G Hughes¹, Nancy F Smith¹, William A Szelistowski¹, Micah Bakenhaster²

¹Eckerd College, St. Petersburg, FL, USA. ²Florida Fish and Wildlife Research Institute, St. Petersburg, FL, USA

Stingrays are common hosts to a variety of marine ectoparasites, yet studies investigating these parasites at the community level are rare. We surveyed Atlantic (*Hypanus sabinus*) and Bluntnose (*Hypanus say*) stingrays in Tampa Bay, Florida, USA, from August to November 2025 to characterise their ectoparasite community. Of the two host species, *H. sabinus* experienced higher parasite prevalence (66.7%) and were infect-

ed by branchiurans (*Argulus flavescens*), copepods (*Caligus* sp. and *Lepeophtheirus* sp.), jawless leeches (*Branchellion ravenelii*), and capsalid monogeneans (*Listrocephalos corona*). Although *Hypanus say* experienced lower prevalence (13.8%), they shared a similar ectoparasite community with *H. sabinus*, serving as hosts to *Argulus flavescens*, *Caligus* sp., *Lepeophtheirus* sp., *Branchellion ravenelii*, and moncotylean monogeneans (*Monocotyle* sp.). Ectoparasites preferred the ventral side of stingrays, with 37.9% of rays being infected on the ventral surface (n = 137 parasites), compared to 24.1% on the dorsal surface (n = 28 parasites), a consistent observation across host species. Parasite load was significantly and positively correlated with body size (ray disc width) for both *H. sabinus* and *H. say*. We compared parasitism between outer and inner regions of Tampa Bay for bluntnose stingrays and found that parasite prevalence and load were significantly higher in the inner bay. Substrate type also had a significant effect on parasitic infection, with Atlantic stingrays experiencing higher infection rates in muddy than in sandy habitats. Additionally, we compared parasites on Atlantic stingrays collected from Tampa Bay with individuals from St. Mark's National Wildlife Refuge and found that the St. Mark's population experienced 1.5x higher prevalence and 13.5x higher load than those in Tampa Bay. However, total species richness was lower in St. Mark's compared to Tampa Bay. Differences in prevalence and parasite load across ray species, locations, and habitats indicate that host lifestyle and environment greatly influence ectoparasitic infections. This study provides a baseline for the relationships between host habitat use and parasitism, which is important in understanding transmission dynamics and managing elasmobranch populations.

100. First report of *Kiricephalus coarctatus* (Pentastomida) in the eastern mud snake (*Farancia abacura*) from Florida

Abigail Arnashus, Oscar Alejandro Aleuy

Florida Atlantic University, Boca Raton, FL, USA

Kiricephalus coarctatus is a North American snake pentastome that exists in Florida's native snake communities via infectivity from intermediate hosts. The Eastern mud snake (*Farancia abacura*) has been documented with the invasive pentastome *Raillietiella orientalis* in Florida, but reports in Florida of *K. coarctatus* do not extend to *F. abacura*, possibly due to a specialized diet of aquatic salamanders. A *K. coarctatus* infection in *F. abacura* from Florida is reported. An adult female *F. abacura* from Broward County, Florida, was collected during road mortality surveys and examined via necropsy. A single immature female *K. coarctatus*, measuring 36 mm, was discovered encysted in the right lung. The *K. coarctatus* specimen possessed morphological characteristics associated with Florida's native snake pentastomes, such as a globular head, two sets of hooks, external annulations, and an oval mouth shape. Molecular confirmation is being conducted to confirm the identity as *K. coarctatus*. This finding represents the first documented case of *K. coarctatus* in *F. abacura* from Florida, and within an Everglades habitat which also hosts the invasive snake pentastome *R. orientalis*. Further investigation is needed to determine infection dynamics in an ecosystem where a native and an invasive snake pentastome exist in sympatry, and the extent to which both pose a conservation risk to Florida's native snakes.

101. Impact of triazicide and atrazine on adult *Paragordius varius*

Oliver J Jensen, John Shea, Sudhanva Kashyap

Creighton University, Omaha, NE, USA

The adult stage of the hairworm, *Paragordius varius* [Nematomorph] may indicate aquatic ecosystem health. Specifically, an indicator of stream health as it relates to the leaching of commercially available chemicals including triazicide (a potent pyrethroid insecticide) and atrazine (a triazine herbicide) into streams. *P. varius* infects 2 different hosts, but its adult stage lives in aquatic environments as a free-floating worm where it is directly exposed to agricultural chemicals such as triazicide and atrazine. If adult *P. varius* worms show a decrease in motility in the presence of agrochemicals (triazicide or atrazine) compared to control worms,

then the decrease in motility will be attributed to the action of these agrochemicals. To test this, *Acheta domesticus* crickets were exposed to *P. varius* cysts and reared to yield adult *P. varius*. Male and female adults were then placed in 1:10 dilutions (10 μ m, 3 μ m, 1 μ m, 300 nm, or 100 nm) of each agrochemical separately in a Phylum Tech WMicrotracker Arena monitoring chamber. Each concentration was tested with a sample size of 2 worms, running both the experimental and control groups simultaneously for 48 hours with a 30-minute normalization period to allow percent motility to be quantified as change in worm motility from baseline. Males exposed to triazicide at 10 μ m and 3 μ m concentrations saw percent motility drops of near 100%, while males exposed to 1 μ m and 300 nm concentrations decreased their motility at near 50%. Roughly the same near 100% motility drop was also seen in females exposed to triazicide at 10 μ m & 3 μ m concentrations. Males and females exposed to atrazine at 10 μ m, 3 μ m, 1 μ m, and 300 nm concentrations showed a 50-100% motility drop on average with the clearest data for males exposed to atrazine at 1 μ m and 300 nm concentrations. Given these results, increasing the sample size would help determine the relevance of utilizing these worms as indicators of stream health and the impact agrochemicals leaching into these ecosystems.

102. Quantifying observer effects in parasite community data

Christopher A Blonar¹, David J Marcogliese²

¹Nova Southeastern University, Fort Lauderdale, FL, USA. ²Environment Canada, Saint Andrews, NB, Canada

To support ongoing meta-analytical studies on the factors that shape parasite communities, we assembled a comprehensive database of parasite diversity in sticklebacks (Gasterosteidae) from published studies and grey literature. To date, this database has already been the foundation of several published studies on distance decay, habitat effects, and infection patterns across spatial scales, but we have also observed an additional pattern: a statistically significant “observer effect” whereby parasite assemblages reported by a given lead author tend to resemble one another both compositionally and structurally. To evaluate the generality of this phenomenon to other databases, we extended our analysis to other publicly available multi-author parasite community data sets covering different host systems and detected a similar effect. The effect size of this “observer effect” can approach that of commonly studied factors such as host phylogeny, phylogeography, climate, habitat, and land use change. This aligns with similar findings in free-living communities, where author-level differences in taxonomic expertise, identification resolution, sampling design, methodological decisions, and analytical framing can shape the resulting species lists. Previous authors have suggested that studies of parasite diversity may be particularly sensitive to observer expertise and methodological variation, as many taxa are difficult to detect, or are cryptic and require specialist identification; consequently, it seems plausible that observed parasite biodiversity patterns should at least to some degree be shaped by the expertise and choices of the parasitologists who study them. In this study we report the effect size of the “observer effect” in selected parasitological databases and suggest practical recommendations for accounting for author-associated variation in meta-analyses, based on lessons learned by ecologists working in free-living systems (e.g. phytoplankton, birds, reef-associated taxa). Recognizing and addressing this potential source of bias may improve the reliability of cross-study syntheses and strengthen inference regarding the ecological drivers of parasite community assembly.

103. Helminth parasite diversity in white suckers across stream ecosystems in Southeast Pennsylvania

Isabella Cimino¹, Elliana Euclide¹, Kevin Stover¹, Elizabeth Hoffeditz², Alexander D. Hernandez²

¹Marine Science Program, Kutztown University of Pennsylvania, Kutztown, PA, USA. ²Department of Biology, Kutztown University of Pennsylvania, Kutztown, PA, USA

Little is known about what the parasites are that naturally infect white suckers, *Catostomus commersonii*, that permanently reside in Pennsylvania streams, how variable the distribution is across the biogeographic range of this fish species, or what biotic and/or abiotic factors impact these variabilities. White suckers are part of cool water fish communities that include minnows such as blacknose dace (*Rhinichthys atratulus*), golden

shiner (*Notemigonus crysoleucas*) and cutlips minnow (*Exoglossum maxillingua*) that reside in small to medium size streams at moderate to relatively high elevation and gradient, with intermediate temperatures between warm and cold-water streams. Previous observations on the diversity and abundance of helminth parasites in a cool water fish community in southeast Pennsylvania indicated that white suckers had the most diverse helminth parasite community with six species, relative to the number of parasite species (between 0 and 3) in minnows and other less common fish species. We were therefore interested in comparing the diversity of the helminth community infecting white sucker from six tributaries in the same watershed, the Schuylkill River, to assess the relative variability between populations. We collected 242 white suckers between October 2023 and December 2025 using a backpack electro-shocker from Willow Creek (n= 55), Sacony Creek (n= 37), Cacoosing Creek (n= 95), and Northkill Creek (n= 9), Manatawney Creek (n= 31), and West Branch Schuylkill River (n=15). A total of 12 helminth genera, species, and/or morphospecies have been identified thus far, with clear differences in species richness and community composition between fish host populations. Our work adds to the limited data available about the composition and diversity of helminth parasite communities infecting white suckers, specifically, and fish species, generally, that reside in Pennsylvania riverine ecosystems. Those data come from fewer than a dozen scientific articles or reports published over the past 160 plus years.

104. A quantitative assessment of ingested microplastic impact on internal parasites in waterbirds

Elizabeth M Bevis, Kate L Sheehan

Frostburg State University, Frostburg, MD, USA

Microplastic pollution poses a significant threat to wildlife, with avian species particularly vulnerable to entanglement, physical injury, and accidental ingestion. While prior research has documented microplastic-associated disruptions to gut microbiomes, tissue integrity, and immune function in birds, significant gaps remain. How these effects manifest across distinct intestinal regions and how microplastics interact with internal parasite communities in waterbirds are key questions we aim to address. Here, we evaluate the endoparasite assemblages among four waterbird species commonly predating products on aquaculture facilities. We have examined Laughing Gull (*Leucophaeus atricilla*), Double-crested Cormorant (*Nannopterum auritum*), Great Blue Heron (*Ardea herodias*), and Great Egret (*Ardea alba*) gastrointestinal tracts collected by USDA/APHIS Wildlife Services cooperators in 2024–2025. Each bird's small intestinal tract is split into its anatomical sections: the duodenum, jejunum, and ileum. Concomitant to parasite assessments in each intestinal section, we collected tissue samples for histological staining (Hematoxylin and Eosin; Masson's Trichrome). We also swabbed each intestinal section for next-generation DNA sequencing of microbial communities. With these samples, we plan to investigate the effects of ingested microplastics on gut microbial communities and intestinal tissue structure. Parasite evenness is likely to increase with species size. Double-crested Cormorants are primarily piscivores suggesting lower parasite diversity given lower diet variety. Here, we provide novel baseline data on the co-occurrence of microplastics and parasites across intestinal regions in two waterbird species, with additional samples from two other species to be assessed in the future.

105. Plastics, poisons, and parasites: The impacts of microplastics on endoparasites in eastern newts

Eric J Jergensen, Kate L Sheehan

Frostburg State University, Frostburg, MD, USA

Microplastics pose a threat to amphibian populations worldwide, as most larvae rely on freshwater habitats to forage and mature. Microplastics can irritate internal organs and trigger the hypersecretion of mucus when consumed by amphibians, potentially impacting other defensive secretions. Eastern Newts (*Notophthalmus viridescens*) return to aquatic life after their terrestrial eft stage, re-exposing them to parasites and microplastics as adults. Eastern Newts also produce tetrodotoxin (TTX), a potent neurotoxin used by amphibians

to deter predators; however, the effects of secreted defenses (such as mucus and toxins) on parasites remain debated. Here, we investigate the impact of consumed microplastics on defensive compound production and endoparasite communities in the skin and intestines of wild-caught adult Eastern Newts. Free-living newts from Western Maryland populations were necropsied to assess microplastic counts, parasitic infections, defensive compound (TTX and mucus) production, microbiome, and morphological data. Here, we present preliminary findings from this survey. Defensive compounds are quantified using immune assays, histology, and immunohistochemistry. We found no relationship between microplastic and endoparasite frequencies (Poisson GLM); however, defensive compound production and microplastic count were positively correlated. Our histological assessments confirmed that, like other newt species, Eastern Newts have glands capable of secreting both mucus and toxin, which supports the strong associations between defensive compound secretions. Despite previous reports of low prevalences of newt endoparasites, we found a 100% prevalence of intestinal helminths. Consistent with previous findings, the presence of endoparasites in chemically defended organs of Eastern Newts suggests resistance to, or perhaps affinity for, TTX in some parasites. This improves our understanding of the effects of environmental contaminants on amphibian defenses against natural enemies and opens the door to further assessments of co-occurring symbiotic communities.

106. Gastrointestinal endoparasite communities of wood-warblers in coastal southeast Florida

Ema P Nagel¹, Christopher A Blonar², David W Kerstetter¹

¹Department of Marine and Environmental Sciences, Halmos College of Arts and Sciences, Nova Southeastern University, Dania Beach, FL, USA. ²Department of Biological Sciences, Halmos College of Arts and Sciences, Nova Southeastern University, Davie, FL, USA

Wood-warblers (Family Parulidae) are a diverse group of primarily insectivorous passerine birds. Within Parulidae, 43 species have been documented in Florida including both resident populations and migratory individuals. Gastrointestinal endoparasites can be abundant in insectivores, and these communities are likely to differ compositionally among parulids with differing foraging strategies. Despite the common presence of parulids throughout North American ecosystems, knowledge of their endoparasite communities remains sparse in current literature. To address this knowledge gap, warbler specimens were opportunistically collected postmortem from 4 collaborating wildlife rescue centers in southeast Florida. Specimens analyzed represent 10 locally common parulid species: American Redstarts (*Setophaga ruticilla*), Black-and-White Warblers (*Mniotilta varia*), Black-throated Blue Warblers (*Setophaga caerulescens*), Cape May Warblers (*Setophaga tigrina*), Common Yellowthroats (*Geothlypis trichas*), Northern Parulas (*Setophaga americana*), Ovenbirds (*Seiurus aurocapilla*), Palm Warblers (*Setophaga palmarum*), Yellow-rumped Warbler (*Setophaga coronata*), and Yellow-Throated Warbler (*Setophaga dominica*). The digestive tracts of 225 birds were extracted and examined for endoparasites microscopically. Utilizing standard staining and mounting procedures, parasites were identified to the lowest possible taxonomic level using dichotomous keys. Phyla Nematoda, Cestoda, and Digenea were prevalent, with further identifications, including, members of subfamily Opisthorchiinae and the genus *Mesocostoides*. By documenting current baselines of parulid endoparasite communities, these findings establish a foundation for future studies while providing additional insights on parasite diversity in relation to host foraging, diet, and ecology; they also can inform ongoing conservation efforts and veterinary treatment by providing baseline documentation of endoparasite diversity and host loads for wildlife rehabilitation facilities.

107. A survey of endohelminths of holosteans in Georgia

Tyler J Achatz¹, Maggie A Young^{1,2}, Zoe Von Holten³, Makala E Fabrizio¹, Caley H Chun¹, M Tyler Harris¹, Nathaniel J Hornung¹, Marion Baker⁴, Jim Page⁴, Brandon Baker⁴, Caroline Cooper⁴, Amory Cook⁴, Laura Wenk⁴, Tim Bonvechio⁴, Don Harrison⁴, Jonathon Pritchard⁴, J Mike Kinsella⁵, Florian B Reyda⁶, Anindo Choudhury⁷, Vasyl V Tkach²

¹Middle Georgia State University, Macon, GA, USA. ²University of North Dakota, Grand Forks, ND, USA. ³Georgia Southern University, Statesboro, GA, USA. ⁴Georgia Department of Natural Resources, Atlanta, GA, USA. ⁵HelmWest Laboratory, Missoula, MT, USA. ⁶State University of New York at Oneonta, Cooperstown, NY, USA. ⁷St. Norbert College, De Pere, WI, USA

Holostean fishes (bowfin *Amia calva* and gars *Lepisosteus* spp.) represent phylogenetically ancient lineages that are widespread in freshwater systems of North America, yet their parasite faunas remain insufficiently documented; this is particularly true for Georgia. In the present study, we surveyed the intestinal helminths of bowfin, longnose gar (*Lepisosteus osseus*), and spotted gar (*Lepisosteus oculatus*) collected from lakes and rivers across three major watersheds in Georgia. A total of 145 fishes (36 bowfin, 40 longnose gar, and 69 spotted gar) were examined. We recovered representatives of Acanthocephala, Platyhelminthes (Cestoda and Digenea), Nematoda, and Pentastomida. In total, 11 helminth taxa were detected in bowfin, 7 in longnose gar, and 11 in spotted gar. The cestode *Laruea perplexa* was the most prevalent parasite in bowfin (61.1%), whereas juvenile *Contracaecum* sp. was the most common parasite in gars (up to 30.4% prevalence). Several digeneans and cestodes exhibited moderate prevalence, whereas many taxa occurred at low prevalence and likely represent accidental infections. More than 10 parasite species are reported for the first time from Georgia. These results substantially expand baseline knowledge of helminth diversity in Georgia fishes and highlight the need for broader parasitological surveys of understudied fish lineages in the region.

108. Examining altered behavior in millipedes (*Spirobolus* sp.) infected with terrestrial hairworm, *Gordius chiashanus*

John F Shea¹, Ming-Chung Chiu²

¹Creighton University, Omaha, NE, USA. ²National Taiwan University, Taipei, Taiwan

To complete their lifecycle, many aquatic hairworms [Nematomorpha] manipulate their terrestrial arthropod hosts into entering water where the adults emerge. Recently, hairworms have been described from terrestrial environments (Anaya *et al.*, 2019 and Chiu *et al.*, 2020) where they are thought to infect large millipedes. Parasite manipulation of hosts may be a conserved trait found in both aquatic and terrestrial hairworm species. Infected millipedes may differ from uninfected millipedes when seeking shelter, avoiding light or burrowing in the ground. Further, they may differ in the depth at which they burrow, especially in the presence of water which may stimulate terrestrial hairworm emergence. To test this, we collected over eighty millipedes (*Spirobolus* sp.) from Xitou Park in Nantou County, Taiwan where the terrestrial hairworm, *Gordius chiashanus*, has been observed infecting these millipedes (Chiu *et al.*, 2020). Millipedes were brought back to the lab on the following day, sorted by size, sexed and stored in 16°C incubators. All surviving millipedes will undergo four behavioral trials to test their preference for shelter, light, burrowing, and burrowing depth in the presence of water. Trials will last 24 hours under constant temperature with data collection occurring every 10 minutes via camera. When relevant, trials will take place 12 hours in the light and 12 hours in the dark. Infection status of each millipede will be determined after all trials have been conducted. We hypothesize that infected millipedes will exhibit altered behavior compared to uninfected millipedes. Results will be discussed considering host manipulation by terrestrial hairworms as well as what we know of the hairworm's lifecycle. Although this study only provides correlational data, it may lead to similar trials involving experimentally infected millipedes to demonstrate cause and effect. If terrestrial hairworms manipulate their hosts like aquatic hairworms manipulate their hosts, then such behavior is conserved in the phylum. Such behavior alterations could also be linked to molecular analysis.

109. “Can I eat this?”: Assessing freshwater fish parasites in the Wisconsin Ceded Territory

Raymond L Allen, Gretchen A Gerrish

University of Wisconsin-Madison - Trout Lake Station, Boulder Junction, WI, USA

The Lac du Flambeau Indian Reservation, located in northern Wisconsin, is home to the Lac du Flambeau Band of Lake Superior Chippewa Indians and to over 250 freshwater lakes containing fish, invertebrates, aquatic plants, and pathogens. The Lac du Flambeau (LDF) Tribe owns and operates the William J. Poupert, Sr. Fish Hatchery, which is responsible for raising and stocking hundreds of thousands of culturally and socially important fish to lakes within the reservation boundaries and throughout the Great Lakes Ceded territory and has duties to assess fish health in the hatchery and reservation lakes. This research, in collaboration with the LDF Fish Hatchery, aims to increase the knowledge of infectious pathogens in fish in area lakes at multiple stages of fish and pathogen development, and begins to address questions on the long-term health of freshwater fish populations in the region in terms of a changing climate, and human-induced changes in lakes. This presentation will talk about the ongoing broad assessment of fish pathogens throughout the regional lakes which is being used to determine what pathogens are present, at what severity, and to determine parasite host development and severity across time. We surveyed harvested walleye and whitefish organs for parasites and seasonal infection rates by microscopy and DNA barcoding, and show our preliminary results.

110. Intestinal parasite communities of invasive cane toads and native southern toads in southwest Florida

Mia R Clement

Florida Gulf Coast University, Fort Myers, Florida, USA

Cane toads (*Rhinella marina*) are highly invasive amphibians native to South America that have caused significant ecological disruption throughout Florida. Despite their impact, relatively few studies have examined the parasite communities of the invasive cane toads or the closely related native Southern toads (*Anaxyrus terrestris*). The objective of this study was to examine parasites found in the gastrointestinal tract of both toad species in Southwest Florida. Toads were collected by an anonymous contractor, delivered frozen to Florida Gulf Coast University (FGCU), and stored at -20°C. Prior to necropsy, individuals were weighed, measured, and sexed. During necropsy, the stomach, intestines (upper, middle, and lower), and colon were separated, placed in petri dishes with water, and examined under a stereomicroscope. Parasites were counted, photographed, measured, and preserved in labeled 1.5 mL microtubes containing 70% ethanol. A total of 35 toads were sampled, including 21 cane toads and 14 Southern toads. Stomach infections were rare in both species, indicating occasional gastric colonization. The upper intestine also showed consistently low parasite presence across both species. Parasite prevalence increased in the middle intestine, where cane toads exhibited 38.1% prevalence with a mean intensity of 26.9 ± 41.7 parasites (range = 1-118), compared to 35.7% prevalence and 9.2 ± 10.5 parasites (range = 1-23) in Southern toads. In the lower intestine, cane toads showed 47.6% prevalence with a mean intensity of 82.4 ± 133.6 parasites (range = 1-431), while Southern toads exhibited 64.3% prevalence and markedly higher intensity of 536.2 ± 781.2 parasites (range: 37-2414). In the colon, parasite loads remained high in both species but were especially extreme in Southern toads, indicating strong posterior gut aggregation. Cane toads harbored higher parasite richness compared to Southern toads. Across both species, parasite abundance followed a consistent spatial pattern, with minimal infection in the stomach and upper intestine, increasing infection in the middle intestine, and highest accumulation in the lower intestine and colon. These results demonstrate that while invasive cane toads support greater parasite diversity, native Southern toads experience significantly higher parasite burdens in posterior gastrointestinal regions, suggesting species-specific differences in parasite distribution and gut habitat suitability.

111. The Spider Parasite Digital Research (SPDR) Collection

Carl N Keiser

University of Florida, Gainesville, FL, USA

Parasitism is the most common lifestyle among animals, arising from over 200 independent evolutionary origins. Yet, it has been predicted that at least 85% of parasite species remain unknown to science - parasites were once described as the “ultimate missing link” of trophic ecology. Spiders are some of the most important invertebrate predators in terrestrial ecosystems, though spiders’ interactions with parasites remain sorely understudied. The Behavioral Disease Ecology Lab at the University of Florida maintains the Spider Parasite Digital Research (SPDR) Collection which serves as a foundational resource for studying parasite biodiversity, digitizing and distributing information freely, and incorporating the active participation of community scientists. The aim of the SPDR Collection is to build a collaborative, fully digitized research collection which houses preserved specimens, photographs, and DNA sequences of spider-parasite specimen pairs in a searchable online database. In keeping both host and parasite together, along with the plant substrate on which specimens were collected, this database serves as both a biodiversity collection and a catalog of ecological interactions. The SPDR collection currently houses samples representing fungal pathogens, parasitoid wasps, ectoparasites, and parasitic nematodes.

112. Necropsy and specimen curation: A parasitological survey of Florida avifauna

Ash Hernandez-Trochez, Malia Tinsley, Oscar Johnson

Florida Gulf Coast University, Fort Myers, Florida, USA

Studying parasite diversity in wild birds provides critical understanding into ecosystem health and wildlife disease dynamics. As indicators of environmental conditions and key players in the food web, parasites offer a unique lens that is used to assess the well-being of host populations. Though avian parasitology is well-studied globally, baseline data for many resident and migratory bird populations in Southwest Florida remain limited, creating a gap in regional understanding of host-parasite dynamics. This survey addresses this gap by using modified necropsy and specimen preparation procedures to document parasite richness and infection rates amongst wild bird specimens donated to the Florida Gulf Coast University Ornithological collection. Bird specimens had been salvaged from roadkill, window strikes, and other mortality events, then frozen immediately at collection. After thawing, bird skins were examined for both external and internal parasites. Following the preparations of museum study skins, a modified necropsy was performed. Organs and body cavities were inspected for parasites visible to the naked eye. Initial results include parasite infection rate per specimens and per bird species, a general identification of parasite type, other pathologies, and unusual growths and organ discoloration. Preliminary findings from 32 bird specimens identified parasites in 25% (8 of 32) of specimens, with nematodes and cestodes being most observed. This research establishes a baseline for future comparative studies on avian parasites in the region and enhances the research value of the FGCU ornithological collection by preserving both specimens and associated parasite data.

113. Species survey of helminth parasites from invasive and native snakes in south Florida

Luke W Niemann

Florida Gulf Coast University, Fort Myers, FL, USA

Despite the invasive Burmese python being established since the 1980s, little is known about their helminth parasites. While a few studies have examined the transfer of a crustacean lung parasite from pythons to native snakes, studies on other parasite taxa are limited. Therefore, we don’t fully understand the impact of other invasive parasites on native snakes. Combined with limited information on parasites of native snakes, we know little about the potential of zoonoses or spillover. Without a baseline of native parasite communi-

ties, detecting spillover will become increasingly difficult as more nonnatives become established in southern Florida. The objective of this study was to compare the diversity, prevalence, and intensity of parasites between native snakes and the invasive Burmese python, while creating a species checklist of recovered parasites. Dead pythons were donated to the university by hunters and native snakes were collected opportunistically as roadkill. Morphometric data was recorded, internal organs were removed, and parasites were collected. Clearing, staining, and scanning electron microscopy were used to identify specimens by keying out diagnostic features and referring to previous literature. Shannon's diversity index was used to compare and characterize the overall native and invasive parasite communities, with pythons showing lower species diversity (0.0784) than native snakes (0.202). Python parasites had low species diversity with high overall parasite prevalence. Nematodes *Kalicephalus* sp., and *Serpentirhabdias* sp. were found in pythons, and were also present in native snakes. In the gastrointestinal tract of pythons, *Kalicephalus* sp. had the highest mean intensity (19.24 ± 29.90 ; range: 1-119), while *Serpentirhabdias* sp. had the highest mean intensity in the respiratory tract of pythons (8.4 ± 13.22 ; range: 1-32), both taxa occurring at a higher prevalence than in native snakes. Burmese pythons (6.3%) had lower pentastome prevalence compared to our 3 native snakes (16.7 – 71.4%) sharing both *Raillietiella* sp. and *Porocephalus* sp. Pythons lacked platyhelminths commonly found in native species. Native snakes had high species diversity, parasite prevalence and parasite loads than invasive pythons. Natives support more diverse parasite communities than pythons, despite higher nematode prevalence. Establishing this baseline provides a critical foundation for future studies monitoring changes in Florida snake communities.

114. A comparative analysis of body condition and immunomodulation as indicators of stress in native and non-native cane toads (*Rhinella horribilis*)

Emma R Ulseth^{1,2}, Jordan T Donini², Matthew S Atkinson¹

¹University of Central Florida, Orlando, FL, USA. ²Florida SouthWestern State College, Naples, FL, USA

Florida is undergoing anthropogenic land use changes. Similar environmental factors have been associated with increased corticosterone (stress hormone) secretion in amphibians. As corticosterone secretion elevates white blood cell counts, neutrophil:lymphocyte ratio (NLR) is commonly used as a proxy for stress in anurans. Cane Toads (*Rhinella horribilis*) are terrestrial anurans native to Central America, invasive in Florida, and known to occupy urbanized environments. Here, we sought to explore the effects of urbanization, invasion, and hemoparasite presence on stress by comparing leukocyte ratios and body condition across different populations of *R. horribilis*. We blood sampled 87 total adult *R. horribilis* from three locations: one urban and another natural site in Southwest Florida, where they are invasive, and one native population from a natural site in Costa Rica. We then compared NLR and Fulton's body condition (K) against sex, hemoparasite presence, and location of capture. We observed that urbanization, not invasion status, was associated with significantly lower body condition ($p = 0.049$) and higher NLR ($p < 0.001$), while the effect of parasite presence on these markers was negligible. Notably, hemoparasites were absent from animals from the invasive range but present in 95% of their native counterparts, suggestive of potential enemy release. The results of our pilot study indicate that even where they have successfully invaded, *R. horribilis* can exhibit impacts from anthropogenic land use changes. This study provides insight into the impacts of urbanization, invasion status, and the presence of parasites from the phyla Nematoda and Apicomplexa on *R. horribilis*.

115. Variabilities in host body size and the abundance of *Lissorchius attenuatus* in white suckers from tributaries of the Schuylkill River watershed

Elliana Euclide¹, Elizabeth Hoffeditz², Alexander D Hernandez²

¹Marine Science Program, Kutztown University of Pennsylvania, Kutztown, PA, USA. ²Department of Biology, Kutztown University of Pennsylvania, Kutztown, PA, USA

Lissorchis attenuatus is a trophically transmitted trematode whose adults reside in the intestinal tract of white sucker, *Catostomus commersonii*, after these fish consume infected aquatic oligochaetes or planaria

containing metacercaria. The diet of white suckers varies with age, with sac-fry feeding on floating or drifting zooplankton before their mouth moves from a terminal position to a ventral position after yolk reabsorption. After which, as juveniles, their diet consists of benthic invertebrates, and as their size increases with maturation, so does the size range for food items they consume. We explored what relation, if any, exists between host body size and infection with *L. attenuatus* infecting white sucker populations that permanently reside in riverine ecosystems. We collected 197 fish between October 2023 and December 2025 using a backpack electro-shocker from four tributaries of the Schuylkill River watershed in southeast Pennsylvania: Willow Creek (n= 55), Sacony Creek (n= 37), Cacoosing Creek (n= 95), and Northkill Creek (n= 9). To describe the relation between host body size and parasite abundance, we compared allometric (power law) and linear models and used a Negative Binomial GLM to account for overdispersion based on the lowest Akaike Information Criteria (AIC). When data from all tributaries was combined, host body size (standard length) was a significant predictor ($z= 5.02$, $p= 0.001$; Nagelkerke's $R^2= 0.202$), with an exponent of $b= 1.49$ ($SE= 0.3$), indicating a hyperallometric relationship that suggests parasites are accumulating disproportionately as hosts grow larger. The exponent b indicates that for every 1% increase in host length, there was roughly a 1.5% increase in the number of *L. attenuatus* adult worms. A low dispersion parameter ($q= 0.267$) was reflective of the highly aggregated nature of the parasite distribution within the white sucker populations sampled. When data from each tributary was modeled separately, host body size was a significant predictor in some, but not all populations. The smaller sample size in one stream aside, it's possible that environmental as well as ecological variabilities between tributaries, may explain the variable relation between host body size and the abundance of *L. attenuatus* in Pennsylvania headwaters.

116. The use of zero valent iron to bind coccidian parasites and magnetic attraction to remove oocysts from water

Madison Eshleman, Cory Petter, Mia Kroll, Karis Dawson, Kasey Burchfield, Matthew Tucker

Lake Erie College of Osteopathic Medicine, Bradenton, FL, USA

Cyclospora cayetanensis is a protozoan parasite responsible for thousands of cases of diarrheal illness annually. Infection occurs by ingestion of resilient sporulated oocysts, which persist for months in environmental sources. Research on *Cyclospora* remains limited because parasites cannot be propagated *in vitro* or *in vivo*, complicating efforts related to detection, recovery, and methodology. Therefore, previous studies have utilized surrogates (e.g. *Eimeria* spp.) that exhibit phylogenetic, structural, and biochemical relatedness to *C. cayetanensis*. Zero-Valent Iron (ZVI) is a novel approach for oocyst removal and detection due to ability to bind pathogens (including *Eimeria* and *Cyclospora*) and its magnetic properties. In this study, we investigated the ability of ZVI to bind *Eimeria* oocysts by varying concentration of ZVI in solution and oocyst inoculum, and by using magnetic attraction. Concentrations of ZVI (10-50% w/v) were inoculated with ~160,000-220,000 *E. acervulina* oocysts and incubated for 5 minutes with shaking. After sucrose floatation and concentration, oocysts were counted by microscopy to assess recovery and grading of ZVI adherence to oocysts. Separately, 343,000-503,000 oocysts were incubated with 10-50% ZVI and exposed to a magnet. The number of oocysts in solution was counted and compared to initial inocula to assess ZVI-dependent magnetic adherence. After sucrose floatation, a higher inoculum of 220,000 oocysts was associated with recovery of 19.9-23.6%, indicating at least ~80% of oocysts were bound by ZVI. The greatest number of ZVI bound oocysts occurred with 40% ZVI. Oocysts were coated with ZVI particles at each concentration (range of 18.4-31.1%), and 40% ZVI coated the most oocysts. However, oocysts exposed to 50% ZVI exhibited the greatest aggregates of ZVI. A dose-dependent relationship was observed between varying ZVI concentrations and oocyst recovery following exposure to a magnet. Oocysts that were inoculated with 10% ZVI solution displayed a recovery rate of 13.10%, which decreased to 2.15% when the ZVI concentration was increased to 50%. These findings illuminate the potential use of ZVI as a surveillance and control tool for coccidian parasites with promising adaptation to *C. cayetanensis*. Future studies will focus on further evaluating magnetic separation methods for recovery of ZVI-bound oocysts from water or produce.

117. Seasonal reproductive strategies and occurrence of symbiotic bacteria on *Gyrincola batrachiensis* (Walton, 1929) infecting green frog tadpoles, *Rana clamitans* (Latreille, 1801) from Wisconsin

Alex Bell, Matthew G Bolek

Oklahoma State University, Stillwater, OK, USA

Nematodes in the genus *Gyrincola* Yamaguti, 1938 infect the gastrointestinal tract of tadpoles and exhibit stadal host specificity, where tadpoles are susceptible and metamorphosed anurans are resistant to infection. In North America, *Gyrincola batrachiensis* has been relatively well studied and has a complex reproductive strategy. Females produce two types of eggs. Thick-shelled eggs are released into the external environment to infect other tadpoles. In contrast, thin-shelled eggs never leave the tadpole's intestine and they are autoinfective, hatching in the tadpole's gut and increasing the number of pinworms in a single tadpole. In addition, *G. batrachiensis* collected from Florida, Nebraska and Oklahoma have been reported to be associated with symbiotic bacteria that grow on their cuticle. However, recent studies across North America indicate that *G. batrachiensis* is a complex of five species and include, *G. batrachiensis*, *Gyrincola armatus*, *Gyrincola gulabrevioris*, *Gyrincola moohsia*, and *Gyrincola pilyolcatzin*. Therefore, it is not clear if all of these species have similar reproductive strategies and associations with symbiotic bacteria as previous studies were most likely not always dealing with *G. batrachiensis*. In this study we collected green frog tadpoles, *Rana clamitans* (N = 120), monthly from single location in Genesee Depot, Wisconsin during February through September and identified their pinworms to the species level using morphological characters. We then evaluated this pinworm population for their seasonal reproductive strategy (prevalence, mean abundance, and egg type) and symbiotic bacteria associations. We found that green frog tadpoles were only infected with *G. batrachiensis*. Prevalence and mean abundance were lowest in February being 35%; 0.75 1.3, and increased each month to a high of 100%; 7.3 2.2 in June. This increase corresponded with the presence of thin-shelled autoinfective eggs in the uterus of worms. In addition, some pinworms were associated with symbiotic bacterial growths on their cuticle surface coat. Importantly, bacterial growths were associated with the anterior region (by the excretory pore), mid body (around the vulva), and posterior region (near the cloaca or anus) of the worms. Differential interference contrast and scanning electron microscopy were used to characterize these bacterial and nematode associations and will be presented.

118. Beyond presence/absence: A framework for classifying pathogen relevance to mortality in stranded odontocetes

Jake R Lighthall, Oscar A Aleuy

Florida Atlantic University, Boca Raton, FL, USA

Infectious diseases are recognized drivers of toothed whale (odontocete) morbidity and mortality, yet the contribution of specific pathogens to stranding outcomes remains difficult to quantify. Case studies of odontocete strandings capture valuable individual-level detail but are rarely standardized beyond narrative descriptions, limiting their use for population-level inference. Pathologists routinely distinguish primary causes of mortality from sublethal findings in individual necropsies, but this judgment is rarely formalized at the pathogen-finding level. We reviewed case-study literature to characterize the role of pathogens in odontocete mortality and determine how often individual pathogens are attributed as drivers of mortality. Systematic searches in Web of Science and Google Scholar yielded 1,432 unique articles, of which 180 met inclusion criteria, spanning 341 individual odontocetes and over 1,900 pathogen-testing data points. Based on the narrative attributions by the original authors, we developed a standardized tiered framework: primary, contributory, incidental, and exposure only, that classifies each pathogen finding by its relevance to mortality. We report attribution distributions for major pathogens of concern in odontocetes, including *Cetacean Morbillivirus*, *Herpesvirus*, *Brucella spp.*, and *Toxoplasma gondii*. Across all positive detections, only 10.1% were classified as primary causes of death, while 49.9% received no attribution from the original authors. Attribution varied by pathogen: *Morbillivirus* was rarely identified as the sole killer (8.8% primary) but was overwhelmingly attributed as contributory (60.3%), while bacteria such as *Photobacterium damsela* were never

classified as primary, and went unattributed in 73.3% of detections. We also test a climate-based mismatch hypothesis that pathogen attribution shifts toward more severe categories when environmental conditions at the time of stranding deviate from regional averages. By building a gradient of pathogen relevance that preserves biological nuance, future necropsy and field data can be integrated and analyzed at spatial and temporal scales, assisting researchers in disease monitoring and management.

119. Environmental drivers and implications of *Perkinsus marinus* infection in the eastern oyster in southeast Florida

Blair Willse, Scott Markwith, Alejandro Aleuy

Florida Atlantic University, Boca Raton, FL, USA

Eastern oysters, *Crassostrea virginica*, are important estuarine species that provide ecosystem services including habitat formation, shoreline stabilization, and water filtration. In Lake Worth Lagoon, a highly urbanized subtropical estuary in southeast Florida, oyster populations have declined substantially over the past decade despite ongoing restoration efforts. One potential contributing factor is dermo disease, caused by the protistan parasite *Perkinsus marinus*, which is known to increase under elevated salinity and temperature conditions. While *P. marinus* is extensively studied in the Gulf of Mexico and the northeastern Atlantic, relatively little is known about disease dynamics in subtropical estuaries along Florida's southeast coast. The objectives of this study are i) to characterize spatial and seasonal patterns in dermo prevalence and infection intensity, ii) to evaluate relationships between environmental conditions and dermo dynamics, and iii) to determine whether disease burden is associated with oyster density and reproductive condition over time. This study uses data generated in a long-term monitoring program to examine environmental drivers of dermo infection and their relationship to oyster reef condition in Lake Worth Lagoon, Florida. Five oysters were sampled monthly across six reefs between 2015 and 2025 and assessed for dermo prevalence and infection intensity using Ray's Fluid Thioglycollate Medium (RFTM) and Mackin scoring. Additional datasets include oyster density, reproductive stage, and environmental variables including salinity, temperature, dissolved oxygen, and chlorophyll-a. Generalized linear mixed-effects models were used to account for repeated sampling and assess potential lagged environmental effects using AIC (Akaike Information Criterion) lag models. Preliminary results indicate that dermo prevalence and infection intensity decreased from 2015 to 2025 and vary among reefs, suggesting temporal and spatial variation in disease dynamics. Infection intensity also showed a positive relationship with the proportion of live oysters at each reef, suggesting reef density may facilitate disease transmission. I predict that reefs exposed to persistently high salinity may experience greater disease burden, while seasonal freshwater inflows will influence oyster condition and disease dynamics differently. Overall, this study will improve understanding of how environmental conditions influence host-parasite interactions in urban subtropical estuaries and may help inform oyster restoration and management strategies in southeast Florida.

120. Conservation and divergence on the neo-Y chromosomes of *Brugia* and *Wuchereria* filarial nematodes

Kevin A Zhou-Hackbarth^{1,2}, Tibeb S Mekonen¹, Eric S Haag¹, Julie C Dunning Hotopp^{2,3}

¹Department of Biology, University of Maryland, College Park, MD, USA. ²Institute for Genome Sciences, University of Maryland School of Medicine, Baltimore, MD, USA. ³Greenebaum Cancer Center, University of Maryland School of Medicine, Baltimore, MD, USA

Most described nematodes, including the ancestor of parasitic filarial nematodes, have XX/XO systems, in which females have two X chromosomes and males have a single X chromosome. In the ancestor of the genera *Brugia* and *Wuchereria*, which include the causative agents of lymphatic filariasis in humans, an autosome fused with the ancestral X chromosome. The resulting neo-X chromosome is comprised of the ancestral X chromosome and the formerly autosomal X-added region (XAR). The homolog of the XAR pairs in opposition to the neo-X during meiosis and is thus inherited in a male-limited manner as a neo-Y chromo-

some. Neo-Y-linked contigs have been identified for *Brugia malayi*, but the gene-poor, repeat-rich nature of the neo-Y has prevented their full assembly. Despite much speculation, it is unresolved whether filarial neo-Y chromosomes play any role in sex determination, development, or male-specific functions. Here we present the identification of neo-Y-linked genomic sequences in *Brugia pahangi* and *Wuchereria bancrofti* and compare them with *B. malayi*. This allowed for the first genomic comparison of homologous degenerate Y chromosomes in nematodes. We find that the neo-Y is more divergent between species than other regions of the genome, yet there are also neo-Y-linked genes conserved between all species examined. These conserved genes are candidates for functions important for male development and reproduction. Additionally, we expect this work to aid future genome assembly, annotation, and population genetic efforts.

121. Proteomic changes in *Naegleria fowleri* induced by lectin-glycoproteins

Suk Yul Jung¹, Seyoung Yang², Eun-Jung Kim³

¹Oakland University, Rochester, MI, USA. ²Namseoul University, Cheonan, Republic of Korea. ³Sanggi University, Wonju, Republic of Korea

Naegleria fowleri, a brain-eating amoeba, mainly causes primary amoebic meningoencephalitis (PAM) through the nose while swimming in river and lake. The most critical concern is the exceptionally high mortality rate associated with amoebic infection, reaching approximately 98%, with only about 4 survivors reported among nearly 200 documented cases. In this context, *N. fowleri* infection is highly acute, and if treatment is delayed, it can rapidly lead to patient death. Therefore, a better understanding of *N. fowleri* pathogenicity at the early stage of host-cell interaction—specifically, the binding of lectins to glycoproteins on the host cell surface—may provide a basis for strategies to inhibit *N. fowleri* infection. In this study, *N. fowleri* was treated with various monosaccharides, including mannose, galactose, and glucose, and the differentially expressed proteins induced by each treatment were analyzed. The differential expression analysis revealed that both mannose and galactose treatments induced relatively modest translational changes at 1 h post-treatment. In the mannose-treated group, 28 genes were significantly upregulated, and 55 genes were downregulated compared to the control, while the majority of genes showed no significant changes. In contrast, galactose treatment resulted in a higher number of downregulated genes (n = 121), suggesting a stronger suppressive effect on gene expression at the early time point. This further confirms that mannose contributes the most to cytotoxicity, binding, and downstream signaling. However, the changes in *N. fowleri* induced by galactose, as used in this study, were also found to be significant.

122. Impact of habitat fragmentation on the population genetics of *Lissorchis attenuatus* infecting white suckers from Pennsylvania streams

Dominick W Ebaugh, Cristen L Rosch, Alexander D Hernandez

Department of Biology, Kutztown University of Pennsylvania, Kutztown, PA, USA

The health of freshwater ecosystems is threatened by anthropogenic stressors such as hydrological modification by dams, but few studies have considered how these types of stressors alter patterns of parasite infection in fish from the Schuylkill River watershed in Pennsylvania. This project aims to measure the impact of habitat fragmentation by dams studying variabilities in the genetic diversity of the most common adult parasite species (*Lissorchis attenuatus*) infecting white sucker fish (*Catostomus commersonii*) collected from a total of two tributaries upstream and two downstream of Lake Ontelaunee and Blue Marsh dams in Berks County. DNA was extracted from 18 adult trematodes to amplify nuclear (28S rDNA and ITS2) and mitochondrial (cytochrome c oxidase I) genes. The primers for polymerase chain reactions (PCR) were designed referencing available data from GenBank that were most closely related to *L. attenuatus* and used to amplify 800 base-pair products for each nuclear gene and a 500 base-pair product for the mitochondrial gene. A total of 26 PCR products from 14 individuals sampled from three of the four streams were confirmed using aga-

rose gel electrophoresis. Sequencing following purification of residual enzymes is ongoing, but successful alignment of genomes from fragmented habitats will help describe the impact of hydrological barriers on the genetic diversity of this parasitic helminth.

123. Using mitogenome analysis of the *Echinostoma trivolvis* species complex to find echinostome trematode barcoding genes

Amy C Gudmundson, [Abigail C Finch](#), Jillian T Detwiler

University of Manitoba, Winnipeg, MB, Canada

DNA sequencing has suggested that the diversity of parasitic trematodes is underestimated due to crypsis (i.e. morphologically indistinguishable, but genetically distinct species). For many species, the cytochrome c oxidase I gene is used to delimit species. However, for echinostome trematodes, this gene appears saturated, and the mitochondrial NADH dehydrogenase 1 (ND1) is a more discriminating gene. However, in some cases, more evidence to distinguish between species and diverged populations is needed. The nominal species *Echinostoma trivolvis* exhibits a wide geographic and definitive host range and consists of 3 distinct genetic lineages that may be cryptic species. However, this is only based on genetic differences from a partial fragment of the ND1 gene and similar morphology between 2 of the 3 lineages. To test the hypothesis of crypsis in *E. trivolvis*, we will use an integrative taxonomy approach. We will use genome skimming (Illumina low-coverage shotgun whole genome sequencing) to obtain mitogenomes from each of the 3 *E. trivolvis* lineages acquired from wild-caught muskrats collected in Indiana, USA (lineage a), Virginia, USA (lineage b), and Manitoba, Canada (lineage c). Mitogenome assembly will be performed by mapping the sequence library of paired reads to a reference *Echinostoma revolutum* mitogenome. Secondary structure of the mitogenome will be determined, and comparison with *E. revolutum* will aid in annotating mitochondrial genes. In addition, we will measure up to 27 morphological characteristics for up to 30 individuals per lineage and perform multivariate analysis to test for morphological differentiation amongst the lineages. Principal component analysis will group the morphological characteristics into distinct clusters. Groups formed by these clusters will be analyzed using linear discriminant analysis to determine the likelihood of misclassification and identify key morphological characteristics that enable discrimination between lineages. Characterizing the mitogenome will determine whether there is mitogenome phylogeny support for the species-level status of cryptic lineages and will help to identify additional genetic markers that may better reflect population and species-level differences. These genetic resources will enable future research on the genetic variation, taxonomy, geographic distributions and host specificity of echinostome trematodes.

124. Investigating mitogenomic variation in *Haemaphysalis* ticks

[Marissa Ohran](#), Rokeya Ahmed, Stephen E Greiman, Dmitry A Apanaskevich

Georgia Southern University, Statesboro, GA, USA

Only a limited number of *Haemaphysalis* tick species occur in North and South America, where adult stages primarily parasitize deer, rabbits, and birds. The genetic diversity and evolutionary relationships of these species remain incompletely understood. In this study, we present mitochondrial genome analyses of selected *Haemaphysalis* species, which reveal notable genetic divergence among sampled populations. This mitogenomic variation corresponds with observed morphological differences, suggesting the potential presence of cryptic diversity within currently recognized species. Although mitochondrial genomes provide an important first insight into population structure, additional data are required to fully resolve taxonomic boundaries. Future analyses incorporating single-copy nuclear genes will be critical for confirming these preliminary findings and for clarifying the evolutionary and taxonomic implications of the combined mitogenomic and morphological divergence.

125. Whiprays in the genus *Maculabatis* (Elasmobranchii: Urogymnidae) as hosts of new species of *Caulobothrium* (Cestoda: “Tetraphyllidea”) sharing a subtle morphological feature

Molly A Kennedy, Kirsten Jensen

University of Kansas, Lawrence, KS, USA

The genus *Caulobothrium* was erected by Baer in 1948 based on Linton’s (1890) description of *Rhinebothrium longicolle* from the spiral intestine of the Bullnose eagle ray, *Myliobatis freminvillei*. The higher classification of *Caulobothrium* is in flux as it remains a member of Clade 4 in the non-monophyletic elasmobranch tapeworm order “Tetraphyllidea”. Presently, there are 10 valid species of *Caulobothrium* recognized. Distinguishing features of this genus include the presence of stalked bothridia with multiple loculi, an apical sucker in the anterior most unpaired loculus, as well as the presence of post-vaginal testes. In addition to eagle rays (Myliobatidae), one described member of *Caulobothrium* is known from a species of cowtail ray (Hypolophidae). Preliminary molecular data suggest the presence of three novel, closely related, species of *Caulobothrium* parasitizing the spiral intestines of whiprays in the genus *Maculabatis*. For this study we examined nine host specimens, representing two described and one potentially novel species of *Maculabatis* (*M. bineeshi*, *M. pastinacoides*, and *M. cf. gerrardi* 6) from three localities across the Indo-Pacific region (India, Malaysia, and Mozambique, respectively). Specimens of *Caulobothrium* consistent with the morphology of the molecular vouchers were recovered from seven host individuals. We used light and scanning electron microscopy to distinguish these new species from previously described species and each other. The three new species share the presence of gladiate spinitriches in a posterior unpaired loculus on each bothridium, a feature not described in any of the 10 valid species. Features of both the scolex and strobila—loculi and proglottid number, as well as total length—distinguish these new species from one another. This work expands the host associations of *Caulobothrium* to include *Maculabatis* and contributes to our understanding of morphological diversity represented in the genus. Further investigation into the species diversity of *Caulobothrium* is warranted, as molecular sequence data from a range of primarily stingray hosts indicate that only a fraction of its diversity is currently described and that its diversity is at least double.

126. Histological evaluation of coccidian parasites in the tropical house geckos, *Hemidactylus mabouia* and evidence for a new genus of lizard coccidia

Allison M Bryant¹, Gabriel J Langford², Matthew G Bolek¹

¹Oklahoma State University, Stillwater, OK, USA. ²Florida Southern College, Lakeland, FL, USA

Classification of coccidia at the generic and family levels was traditionally based on the life cycle and the number of sporocysts and sporozoites in the exogenous stages (oocysts). The genus *Eimeria* reported from all vertebrate classes was defined by tetrasporocystic, dizoic exogenous oocysts. However, recent molecular and developmental studies on eimeriid coccidia, support multiple lineages of coccidia with tetrasporocystic, dizoic oocysts. Two of these lineages, *Choleoeimeria* and *Acroeimeria*, found in reptiles, contain a suture on the sporocyst and epicytoplasmic development in the gall bladder or intestine and are considered phylogenetically distant from the genus *Eimeria* which infect birds and mammals and contain stiedal bodies on the sporocyst. However, there are several species of *Eimeria*-like coccidia from reptiles, which excyst via the suture in the sporocyst wall but contain intracytoplasmic development. These taxa do not fit the definition of *Eimeria* nor the definition of the genera *Choleoeimeria* or *Acroeimeria*. However, no sequence and/or histological data is available for these *Eimeria*-like coccidian. It is unclear if they represent a currently undescribed *Eimeria*-like genus or should be included in *Choleoeimeria* or *Acroeimeria*. To address this issue, we examined the introduced tropical house gecko, *Hemidactylus mabouia*, from Florida for coccidia infections. The oocyst morphology and endogenous development were documented and partial 18s rRNA sequences were obtained. The phylogenetic analyses of all available 18s rRNA sequences and histological data of *Eimeria*-like coccidia species from New and Old-World lizard species indicated three clades that differed in site of infection (gall bladder or intestine) and development (epicytoplasmic or intracytoplasmic). The analysis strongly suggests that a third *Eimeria*-like genus of coccidia infects lizard hosts. This work supports previous

work that oocyst morphology is not useful in differentiating between these genera and obtaining oocyst morphology, endogenous development, and sequence data in future *Eimeria*-like species descriptions will be critical in the understanding of their taxonomical position and phylogenetic relationships.

127. Do tongueworms (Mandibulata: Pancrustacea) retain two pairs of vestigial antennae? A comparative scanning electron microscopy study

Matthew G Bolek¹, Allison Bryant¹, Gabriel Langford², Ryan Koch³

¹Oklahoma State University, Stillwater, OK, USA. ²Florida Southern College, Lakeland, FL, USA. ³University of Pennsylvania, Kennett Square, PA, USA

Pentastomes, or tongueworms, are a neglected and poorly studied group of endoparasites with about 130 described species. As adults, they infect the respiratory tract of vertebrates, and the majority of species grow to maturity in the lungs. These parasites use crocodilians, lizards, snakes, and turtles as definitive hosts, with a few species infecting amphibians, birds, and mammals. The affinities of tongue worms have long proved controversial. However, studies on their sperm morphology and recent molecular studies indicate they are endoparasitic crustaceans and closely related to ectoparasitic crustaceans known as fish lice (Branchiura). As a result of their endoparasitic lifestyle, tongueworms are vermiform in shape, with a conspicuously annulated abdomen, rounded cephalothorax, and a reduction of crustacean appendages to five anterior appendages. These appendages include the mouth and two pairs of hooks, which they use to attach to the host. Studies on larval pentastomes within eggs suggest that they possess two pairs of antennae. However, few detailed scanning electron microscopy (SEM) investigations exist for most adult pentastomes, and vestigial antennae have never been reported in adult tongueworms. Here, we examine six species of pentastomes from five genera (*Raillietiella*, *Sebekia*, *Levisunguis*, *Porocephalus*, and *Armillifer*), from four of eight families (Cephalobaenidae, Sebekidae, Porocephalidae, and Armilliferidae) and both orders (Cephalobaenida and Porocephalida), and compare their cephalothorax anatomy to SEM studies on the cephalothorax anatomy of the related fish lice in the genus *Argulus*. Our results show a surprising similarity of number of appendages on the cephalothorax of the more primitive pentastomes (Order Cephalobaenida) including two pairs of sensilla, the mouth, and two pairs of hooks which appear to correspond to the location of the first and second antennae, the mouth, and the first and second maxillae on the cephalothorax of *Argulus* species. We discuss future studies on how to evaluate if these pentastomid sensilla are homologous to the two pairs of crustacean antennae.

128. Re-evaluation of *Prohemistomum* and related cyathocotyliids (Digenea: Diplostomoidea)

Tyler J Achatz¹, Brooke Ramsingh¹, Maggie A Young^{1,2}, Jonathon Pritchard³, Matthew Keel³, Vasyl V Tkach²

¹Middle Georgia State University, Macon, GA, USA. ²University of North Dakota, Grand Forks, ND, USA. ³Georgia Department of Natural Resources, Atlanta, GA, USA

The taxonomy of the cyathocotyliid genera *Linstowiella*, *Paracoenogonimus*, and *Prohemistomum* has long been unstable, with generic boundaries historically defined by variable morphological characters such as the presence of a ventral sucker. As part of a biodiversity survey of avian helminths in Georgia, we collected numerous cyathocotyliid digeneans from ospreys (*Pandion haliaetus*) representing two genera (*Prohemistomum* and *Neogogatea*). These digeneans were used for morphological and molecular study. Morphological comparisons revealed substantial overlap in diagnostic characters traditionally used to separate *Linstowiella*, *Paracoenogonimus*, and *Prohemistomum* (including the presence or absence of ventral sucker). Additional observations of *Neogogatea kentuckiensis* demonstrated intraspecific variability in the development of the ventral sucker, demonstrating the limited systematic value of this character. Fragments of the large ribosomal subunit (28S) rDNA and cytochrome c oxidase subunit I (cox1) mtDNA gene were sequenced from our cyathocotyliid specimens. Phylogenetic analyses based on 28S sequences demonstrated the position of the collected *Prohemistomum* sp. amongst other cyathocotyliids. We use the combined morphological and molecular data to assess the validity of *Linstowiella*, *Paracoenogonimus*, and *Prohemistomum*.

129. Exploring the phylogenetic affinities of dicrocoeliids with preacetabular testes

Nathaniel J Hornung^{1,2}, Maggie A Young^{1,3}, Tyler J Achatz¹, Rafe M. Brown⁴, Vasyl V Tkach³

¹Middle Georgia State University, Macon, GA, USA. ²University of New Mexico, Albuquerque, NM, USA. ³University of North Dakota, Grand Forks, ND, USA. ⁴University of Kansas, Lawrence, KS, USA

The Dicrocoeliidae Looss, 1899 is a diverse, cosmopolitan family of digenean trematodes that includes 47 genera and over 400 species. Most species are found in avian and mammalian definitive hosts where they commonly parasitize the liver or gall bladder. However, some species parasitize reptilian definitive hosts. While the anatomy of dicrocoeliids is quite variable across the group, the vast majority of genera are characterized by postacetabular gonads. Only a few genera (such as *Euparadistomum* Tubanguí, 1931 and *Proacetabulorchis* Gogate, 1940) have testes positioned anterior to the level of the ventral sucker. However, no genus with the latter state has been included in a phylogenetic analysis of the family. We found and described new species of *Euparadistomum* and *Proacetabulorchis* from lizards in the Philippines and wading birds in Australia. We provide morphological descriptions and differentiation of both species and explore their phylogenetic affinities using partial large ribosomal unit (28S) sequences. Among other results, the molecular phylogeny has revealed that preacetabular position of testes has evolved more than once in the evolutionary history of the group.

130. First report of a monogenoid infecting bighead carp, *Hypophthalmichthys nobilis* (Richardson, 1845) (Cypriniformes: Xenocyprididae) in the United States with phylogenetic analysis and inventory of parasites infecting invasive fishes in the United States

John H Brule¹, Kamila Cajiao-Mora², Daniel Gordillo-González¹, Santiago Escobar-Alfonso¹, Matthew L Horton³, Kelly Winningham⁴, Stephen A Bullard¹

¹Auburn University, Auburn, AL, USA. ²Auburn University, A, AL, USA. ³Arkansas Game and Fish Commission, Little Rock, AR, USA. ⁴Arkansas Game and Fish Commission, Hot Springs, AR, USA

Exotic parasites of exotic, invasive fishes concern fisheries managers, fish culturists, and fish disease diagnosticians because they comprise potential introduced pathogens that can harm cultured hosts and could theoretically harm sympatric wild fishes. Despite the concern of invasive fishes and their parasites in North America, few parasites are reported from invasive fishes there. In the US, silver carp, *Hypophthalmichthys molitrix* (Valenciennes, 1844) and bighead carp, *Hypophthalmichthys nobilis* (Richardson, 1845) (both Cypriniformes: Xenocyprididae) have been introduced into the Mississippi River Basin. Native to Asia, these carps were originally introduced into the US to control algae in aquaculture ponds and wastewater treatment facilities. Herein, bighead carp were gill-netted in the Cache River, Arkansas in May of 2025 by the Arkansas Game and Fish Commission's Invasive Carp Removal Program. We collected an exotic, ectoparasitic flatworm species of *Dactylogyrus* (Platyhelminthes: Monogeneoidea: Dactylogyridae) infecting the gill rakers. Dactylogyrids were heat killed, fixed in 10% neutral buffered formalin, stained, permanently mounted on glass slides, and illustrated under a compound microscope equipped with DIC optical components and a drawing tube. Additional specimens were preserved in 95% EtOH, sequenced (28S rDNA gene and *ITS1*), and included in maximum likelihood phylogenetic analyses. The present study is the first report of a monogenoid infecting bighead carp in North America. This report highlights the under-sampling of invasive fishes for parasitic infections in North America.

131. Expanded records of North American avian cyclophyllideans

Sydney E Horan, Janine N Caira

University of Connecticut, Storrs, CT, USA

Reports of cyclophyllidean tapeworms from North American birds are relatively sparse in the literature. A project aimed at stabilizing and digitizing the parasite specimens in 9 historical collections of parasites housed,

but not yet accessioned into, the Lawrence R. Penner Parasite Collection in the Biodiversity Research Collections at the University of Connecticut prompted investigation of the cestodes of North American birds collected by Larry Penner and his students and colleagues from 1939–1983. Complimenting his slides and vial specimens, his collection includes individual cards providing data on each host specimen necropsied. Of the more than 10,000 necropsy cards, 2,481 were of birds. Examination of these cards and ~150 boxes of microscope slides indicates that the collection includes cestodes from as many as 99 species of birds. Families reported on necropsy cards or represented by his slides include the Davaineidae, Dilepididae, Hymenolepididae, and Paruterinidae. These specimens were primarily collected from Connecticut and Florida and appear to represent new North American localities of a diversity of cyclophyllidean taxa. Likely because of Penner's connections with hunters, the American Black Duck, White-winged Scoter, and Red-breasted Merganser are among the most numerous hosts of cestodes from Connecticut. Less common, but perhaps more interesting are cestodes from the Glossy Ibis, White Ibis, and American Robin. The ultimate goal of the larger project is to digitize all 9 collections and make their existence and associated data publicly available in the Lawrence R. Penner Parasitology Collection portal (lrpennerdb.uconn.edu).

132. Gastrointestinal parasite community of the invasive brown anole (*Anolis sagrei*) in southwest Florida

Eleni G Ryczek, Christina Anaya

Florida Gulf Coast University, Fort Myers, Florida, USA

Invasive species have become increasingly prevalent in Florida due to their rapid population growth and ability to outcompete native species. Beyond displacing native species from their niches, invasive hosts may introduce novel parasites or acquire native parasites, potentially disrupting host-parasite dynamics. The brown anole (*Anolis sagrei*) was first introduced to Key West via international trade in the late 1800s. Since their introduction, they have spread throughout Florida, with subsequent arrivals occurring through the pet trade and cargo shipments. Despite their widespread presence in Southwest Florida, little research has been done on the parasite fauna of this species or whether they may be transmitting parasites to native lizards. The objective of this study was to characterize the gastrointestinal parasite community of *A. sagrei* and establish a baseline parasite checklist for this invasive host. During May – June 2025, a total of 44 anoles including 26 males and 18 females were collected from Florida Gulf Coast University and stored frozen until necropsy. After being thawed, the snout-vent length (cm), mass (g), and sex of each anole were recorded. At necropsy, the organs were isolated into individual petri dishes and examined for parasites. Any parasites found were sorted by taxonomic group and stored in 70% ethanol for further morphological analysis. Parasites preserved in ethanol were analyzed through DNA sequencing, scanning electron microscopy, and mounting for light microscopy when appropriate. Overall, we found four nematode species and one trematode species. The most common was *Physaloptera* sp. which had a prevalence in males (77.8%) that was not significantly different than females (75%; Fisher's exact test, $p = 0.15$). The mean intensity of *Physaloptera* sp. was higher in females (77.3 ± 67.5 ; range 4–137) than males (46.3 ± 44.8 ; range 1–111); although not significantly (t-test, $p = 0.15$). Ongoing analyses will further resolve parasite identifications. This survey is one of the first to document the parasites found in *A. sagrei* from Southwest Florida. Establishing baseline data is essential for interpreting host-parasite dynamics of invasive species and their ecological impacts, including the potential for parasite introduction, spillover, or spillback to native species.

133. When parasites invade the invader: Lung parasites in the Burmese python

Matthew Stutler, Christina Anaya

Florida Gulf Coast University, Fort Myers, FL, USA

Burmese Pythons (*Python bivittatus*) are an invasive species that has introduced the nonnative pentastome parasite *Raillietiella orientalis* to southwest Florida, possibly having detrimental effects on native species. Although the existence of these parasites is well documented, there is limited research on the types of parasites infecting

Burmese pythons and the potential ecological consequences of these infections. The objective of this survey was to examine the parasites inside the lungs of invasive Burmese pythons in Southwest Florida. Burmese pythons were received frozen and placed into a -20°C freezer until necropsy. After defrosting, pythons were measured, weighed, examined for ectoparasites, then opened to remove the respiratory tract. The lungs were separated, placed in a petri dish, and examined for parasites. If parasites were found, they were removed, photographed, measured, and placed into 70% ethanol for later analysis. In the lungs of 22 different pythons, 12 males and 10 females, three different species of parasites were found: two pentastomes and one nematode. One of the pentastomes was identified as *R. orientalis*, and the other to *Porocephalus* sp. *R. orientalis* and the *Porocephalus* sp. each exhibited the same prevalence in female pythons (20%) and in male pythons (17%). However, *Serpentirhabdias* sp. exhibited a higher prevalence in males (25%) than in females (10%). Mean intensity of *R. orientalis* was 2.00 per male and female. Mean intensities for *Porocephalus* sp. in infected females (4.00 ± 3.00 ; 1 – 7) was higher than in males (1.50 ± 0.50 ; 1 – 2). Mean intensities of females infected with *Serpentirhabdias* sp. (3.00) was higher than in males (1.33 ± 0.47 ; 1 – 2). We found that the host mass had an insignificant positive correlation between both parasite length and width of *R. orientalis* ($p = 0.07$) and *Serpentirhabdias* sp ($p = 0.37$), showing a trend of the larger the host the larger the parasite. To the best of our knowledge – this is the first report of *Serpentirhabdias* sp. in Burmese pythons from Florida. Our data shows some of the first steps to creating a list of all the parasites infecting Burmese pythons and how they affect the ecosystem.

134. Parasite diversity in the southern black racer (*Coluber constrictor priapus*) of southwest Florida

Fernanda M Cortazar Penalba, Christina Anaya

Florida Gulf Coast University, Fort Myers, FL, USA

The Burmese python, *Python bivittatus*, was introduced to Florida via the exotic pet trade, and became an established invasive species in the late 1990's. Through their establishment, they have introduced foreign parasites, such as *R. orientalis*, which have spilled over into the native snake population. Though pythons have been avidly studied in Southwest Florida, fewer research has been conducted on parasitism in native snakes. Understanding the parasites infecting native snakes, such as the Southern Black Racer (*Coluber constrictor priapus*), may be essential to mitigating the impact of invasive parasites on native ecosystems. This survey aimed to document parasites found in *C. constrictor* in Southwest Florida. Seven *C. constrictor* specimens were donated anonymously to the FGCU and stored at -20 °C. Each snake was sexed, weighed, and measured. Specimens were necropsied, and the respiratory and digestive organs were placed in petri dishes and inspected for parasites. Found parasites were grouped morphologically, counted, imaged, measured, and identified. Prevalence (P) and mean intensity (MI) were calculated for each parasite species. Seven parasite taxa were collected across four phyla. The most prevalent species were *Physaloptera* spp. (phylum Nematoda), a gastrointestinal nematode seen in 100% of hosts (MI = 18.0, 5 – 43), followed by a pentastome (phylum Arthropoda), *Raillietiella* spp. (P = 71.4%, MI = 22.6, 0 – 67), Acanthocephala (P= 42.9%, MI = 32.6, 1 – 91), GI nematode *Kalicephalus* spp., and cestode (phylum Platyhelminthes), (P = 28.6%, MI = 22.0, 0 – 43 and P = 28.6%, MI = 6.0, 0 – 8, respectively). The least prevalent groups were the respiratory nematode *Serpentirhabdias* spp. (P= 14.2%, MI= 15.0, 0 – 15) and a trematode group (P= 14.2%, MI= 3.0, 0 – 3). Male hosts exhibited a higher parasite richness ($n = 4.0 \pm 0.58$ SE) than female hosts ($n = 2.25 \pm 0.25$ SE), although this was not statistically significant (Welch's t-test, $t = 2.78$, $p = 0.069$). *Physaloptera* spp. collected in male hosts were longer than in female hosts (one-way ANOVA, $F = 9.45$, $p = 0.029$). These findings may provide a baseline for future research on parasite transmission and ecosystem health in Southwest Florida.

135. Under the scales: A parasite survey of the Mediterranean house gecko in southwest Florida

Noah Lewis, Christina Anaya

Florida Gulf Coast University, Fort Myers, FL, USA

Hemidactylus turcicus is a species of house gecko from the Mediterranean and the Middle East but was introduced to Florida in the early twentieth-century international pet trade. The geckos quickly adapted to the region and began a geographical spread accompanied by rapid reproduction. They have also developed a synanthropic lifestyle where they may risk transmitting their parasites to both humans and pets, however, few studies have cataloged the parasites within geckos from Southwest Florida. The objective of this study was to create a checklist of parasites in *H. turcicus* from Southwest Florida. Thirty-eight geckos including twenty-four males and fourteen females were collected opportunistically from the FGCU campus by anonymous donors and stored at -20 °C. The geckos were weighed and measured using snout-vent-length and tail-length. Their skin was first examined for ectoparasites followed by extraction of organs along the respiratory and digestive tracts. Individual organs were separated into 100 mm petri dishes and viewed under a stereo microscope. Any parasites found were extracted from the tissue, sorted by phylum and class using morphology and stored in 70% ethanol. The parasites were then measured/analyzed followed by a combination of DNA sequencing, scanning electron microscopy, and light microscopy. We found four species including one cestode and three nematodes. The cestode *Oochoristica* sp. was found in 26.3% of geckos but more frequently in females (28.6%) compared to males (25.0%) and had a higher mean intensity in females (9.8 ± 20.18 ; 1–51) than in males (2.3 ± 1.50 ; 1–4). Of the nematodes, genus *Parapharyngodon* sp. was the most prevalent being found in 50% of hosts with a higher prevalence in females (57.1%), compared to males (41.6%) and had a higher mean intensity in females (4.4 ± 3.05 ; 1–10) than in males (2.0 ± 0.82 ; 1–3). Identification of remaining taxa is ongoing and will be discussed. This survey is one of the first attempts to catalog the parasite profile of the Mediterranean house gecko within Southwest Florida. The findings from this survey can be used to inform and mitigate possible zoonotic spillovers into humans and pets.

136. Determination of rat lungworm hotspots in Georgia

Caley H Chun¹, Maggie A Young^{1,2}, Jim Page³, Matthew Rowe³, Caroline Cooper⁴, Laura Wenk³, Jonathon Pritchard³, Vasyi V Tkach², Tyler J Achatz¹

¹Middle Georgia State University, Macon, GA, USA. ²University of North Dakota, Grand Forks, ND, USA. ³Georgia Department of Natural Resources, Atlanta, GA, USA. ⁴Georgia Department of Natural Resources, Macon, GA, USA

The rat lungworm, *Angiostrongylus cantonensis*, is an invasive nematode that parasitizes a variety of vertebrates and invertebrates throughout its life cycle. A variety of gastropod mollusks act as the required intermediate host of this nematode, including invasive apple snails (*Pomacea* spp.) and mystery snails (*Heterogen* spp.). A variety of other animals may support transmission by acting as paratenic hosts (e.g., freshwater crustaceans, flatworms, and fish for short periods of time). Infective nematode larvae may also be found on vegetation and in water exposed to infected mollusks. The definitive hosts (rodents) and dead-end hosts (birds, humans, other mammals) become infected by ingesting the larval nematodes. When the nematode larvae are ingested by rats, the nematodes reach the brain, molt, and then migrate to the lungs. In dead end hosts, the nematodes will reach the brain but not adequately develop leading to various neurological pathologies. Rat lungworm has only been reported in Georgia twice. The first time was based on infected rats in the Atlanta Zoo. We provided the second report in the state and demonstrated the parasite to be broadly distributed statewide. In the present study, we collected additional apple snails from southern Georgia to assess potential changes in infection prevalence. In addition, we examined intensities of rat lungworm infections in apple and mystery snails to determine which waterbodies had the most infected snails (i.e., parasite hotspots).

137. Infection patterns of parasitic isopods in marine fishes in southeast Florida and the Florida Keys

Jasmine M Silvennoinen^{1,2}, Ariel J Poholek³, O Alejandro Aleuy¹

¹Florida Atlantic University, Boca Raton, FL, USA. ²FWC Fish and Wildlife Research Institute, Jupiter, FL, USA.

³National Marine Fisheries Survey / National Oceanic and Atmospheric Administration, Key Largo, FL, USA

Parasitic isopods are common crustacean ectoparasites that can influence fish health, population dynamics, and fisheries. *Rocinela signata* (Cymothoida: Aegidae), commonly referred to as the “monogram isopod”, is distinguished by a characteristic “M”- shaped marking on its telson, and occurs in subtropical and tropical coastal waters of the western Atlantic Ocean. Although other parasitic crustaceans are present in this region, *R. signata* is the most frequently reported species in southeast Florida and the Florida Keys, where it commonly parasitizes the gills of marine fishes; however, existing local and regional documentation remains largely limited to host- and location-specific records. This study evaluates how host species, spatial variation, and catch composition influence *R. signata* infection patterns in recreational fisheries catches. Fisheries-dependent data was collected from September 2023 to the present across ~300 miles of coastline in southeast Florida and the Florida Keys through the Southeast Region Headboat Survey, a long-term state and federally supported recreational monitoring program. Fish retained from for-hire vessels were inspected to quantify the number of isopods found on the gills and body surface of sampled fish, and fish hosts were categorized into ecological groups (reef-associated, coastal pelagic, offshore pelagic). Across >124 fish species inspected, over 30 species were positive for *R. signata*, indicating a broad host-range potential. However, initial analyses revealed substantial variation in prevalence among host species and across spatially distinct fishing areas. Among consistently sampled species, prevalence was highest in jolthead porgy (*Calamus bajonado*, 26.3%), followed by mutton snapper (*Lutjanus analis*, 24.1%), and littlehead porgy (*Calamus proridens*, 6.7%). Infection prevalence differed among ecological groups, with reef-associated fish exhibiting significantly higher prevalence than coastal and offshore pelagic groups. These findings support that *R. signata* infection patterns are structured by host species, spatial variation, and ecological grouping. We highlight the need to further investigate cryptic species and genetic diversity, emphasizing the value of integrating parasite monitoring with long-term fisheries surveys.

138. *Echinococcus* in Canada and the United States: Multi-host transmission and spatial distribution

Tajul Islam Mamun, O Alejandro Aleuy

Florida Atlantic University, Boca Raton, FL, USA

Echinococcus spp. are parasitic tapeworms of zoonotic concern in the United States and Canada, with evidence of continued geographic expansion across North America. The objective of this study was to integrate data on host species, spatial distribution, and phylogenetic evidence of *Echinococcus spp.* to better understand its current status in North America. To do this, we conducted a systematic review that included 55 published studies from the USA and Canada and analyzed relevant publicly available genetic sequences from GenBank. Prevalence estimates were calculated using a random-effects meta-analysis with 95% confidence intervals. The overall prevalence of *Echinococcus spp.* across wild species was 18.19% (9.59–31.81%) in Canada and 8.72% (5.18–14.29%) in the USA. Species-specific prevalence estimates in wild hosts were 12.35% (8.18–18.61%) for *E. multilocularis*, 7.07% (3.78–14.20%) for *E. canadensis*, and 6.90% (5.29–8.96%) for *E. granulosus*. Host-level patterns of *Echinococcus spp.* showed clear differences in prevalence among host groups, with canids – particularly coyotes (16.38%, 11.78–22.32%) and red foxes (18%, 11.40–27.98%) – serving as primary definitive hosts, while intermediate hosts, including rodents (e.g., deer mice), exhibited lower prevalence (5.04%, 2.37–10.42%). The prevalence among domestic dogs was 1.00% (0.00–2.00%). The geographic distribution of *Echinococcus spp.* varied across geographic regions, likely reflecting non-probabilistic sampling approaches, with prevalence hotspots identified in Alaska and across northern and central Canada, including Alberta, Saskatchewan, and Manitoba, as well as in the north-central United States, particularly North Dakota. Human cases remain rare in the USA, but spatially overlap in Canada with high-prevalence *Echinococcus* regions, indicating a persistent zoonotic risk. Phylogenetic analysis of *E. multilocularis* revealed clear geographic clustering, with the spatial distribution of several European lineages. This finding

is consistent with previous studies and indicates recent introductions and/or ongoing evolutionary dynamics. Overall, the results of the study may contribute to a better understanding of the current status of echinococcosis in North America and may be useful for controlling the disease in endemic areas.

139. Reemergence, or rediscovery, of common liver fluke (*Fasciola hepatica*) in Wyoming, USA

Lauren E Camp, Jesalynn Borgman, Katie D Bardsley, Ali Brower

University of Wyoming/Wyoming State Veterinary Laboratory, Laramie, WY, USA

Common liver flukes, *Fasciola hepatica*, have been considered endemic in Wyoming (WY) since 1951 and have been documented from WY ruminants periodically over the last 75 years. Sheep and cattle producers in WY currently do not have much awareness of liver fluke as a cause of disease in their herds, despite recent confirmed cases in cattle from the middle of the state. Clinicians in WY are more aware of *F. hepatica*, but it may not be high on their list of rule-outs for disease in livestock. The presumed lack of awareness has resulted in few to no submissions from cattle and sheep for diagnostic tests most appropriate to detect *F. hepatica*. This presentation will describe specifics of the confirmed cases in WY cattle and document efforts to raise awareness among producers of both the continued presence of this parasite in WY and how to submit samples to detect this parasite. Additionally, this presentation will outline plans for *F. hepatica* surveillance in WY using animal (fecal) and environmental (snail) samples.

Author Index by Abstract Number

A

Abagero, Beka Raya **41**
 Abbas, Dawood **42**
 Abugri, Daniel 18, **52**, 73, 74
 Achatz, Tyler 7, **36**, 76, 107, **128**,
 129, 136
 Achi, Perla 10
 Adema, Coen 75
 Aderogba, Moses 87
 Adhvaryu, Het 44
 Agbana, Temitope 87
 Ahmed, Rokeya 12, **13**, 76, 124
 Ajakaye, Oluwaremilekun 87
 Ajisere, Adam Temitope **18**
 Akinbo, Frederick 87
 Akinbo, Yetunde 87
 Aleuy, Alejandro 100, 118, 119, 137,
 138
 Algrem, Declan 53
 Allen, Raymond **109**
 Amanyi-Enegela, Juliana 87
 Ambrosio, John 79
 Amporful, Theophilus 36
 Anaya, Christina 45, **80**, 132, 133,
 134, 135
 Apanaskevich, Dmitry 13, 124
 Ardelean, Ana 69
 Arnashus, Abigail **100**
 Arroyo-Torres, Irvin **25**
 Atkinson, Matthew 28, **82**, 114

B

Bae, Eric 29
 Bakenhaster, Micah 99
 Baker, Brandon 7, 107
 Baker, Marion 7, 107
 Baniya, Anil 10
 Bardsley, Katie 139
 Barneche, Jorge 36
 Barnhill, Michaela **49**
 Barrow, Lisa 25
 Barta, John 32, 43, 60, **71**
 Bavier, Lanie 10
 Bayegun, Adedotun 87
 Beane, Jeff 2, 98
 Beebe, Kathryn **19**
 Bell, Alex 63, **117**
 Bell, David 87
 Bennett, Jerusha 8
 Bernot, James 3, 5, 33, **35**

Best, Jessica 46
 Bevis, Elizabeth **104**
 Bird, Jordan 44
 Blonar, Christopher 27, 48, 50, 93,
102, 106
 Blasco-Costa, Isabel 36
 Bodet, Colin 52
 Bolek, Matthew 47, **63**, 117, 126, **127**
 Bonvechio, Tim 107
 Borgman, Jesalynn 139
 Bowlin, Anne 44, 72
 Brant, Sara **16**, 25, 63, 85
 Brinkworth, Amanda 58
 Brower, Ali 139
 Brown, Justin 78
 Brown, Rafe 129
 Brule, John 11, 14, 34, 37, 130
 Bryant, Allison **47**, **126**, 127
 Bueno, Veronica **84**
 Bullard, Stephen 11, 14, 15, 34, 37, 130
 Burchfield, Kasey 116
 Buschang, Katherine **8**
 Byrum, Stephanie 44

C

Caira, Janine 29, **57**, 84, 131
 Cajiao-Mora, Kamila 14, **37**, **130**
 Calhoun, Dana **55**, **76**
 Camp, Lauren **139**
 Carmona-Yong, Grace 25
 Carneiro, Matheus Batista 72
 Carpenter, Nichole 36
 Carr, Mckayla 95
 Chapman, Olivia 12
 Chaudhari, Sujata 58
 Chen, Hsuan-Wien **61**, **81**
 Childress, Jasmine 9
 Chiu, Ming-Chung 108
 Choi, Young-Jun 17
 Choudhury, Anindo 7, 107
 Chun, Caley 107, **136**
 Cielocha, Joanna 48
 Cimino, Isabella **103**
 Clement, Mia **110**
 Clopton, Debra 77
 Clopton, Richard **77**
 Coers, Jörn 44
 Cohen, Beth **43**
 Cook, Amory 7, 107
 Cooper, Caroline 7, 107, 136
 Cortiñas, Roberto 58

Courts, Kielee 10
 Cove, Michael 98
 Criscione, Charles 30, 70
 Cromwell, Kara 76
 Curran, Stephen 14, 34, 37

D

Dalling, Ness 22
 Darabus, Gheorghe 69
 Dawson, Karis 116
 Deets, Gregory 3
 Deinhart, Molly **97**
 Dennee, Layla 25
 Detwiler, Jillian 1, **22**, 123
 Diehl, Jean-Carel 87
 Dillman, Adler 10
 Dini, Mahya 89
 Donini, Jordan 114
 Dumetz, Franck 41
 Duncan, Kathryn 58
 Durkin, Emily **79**
 Durland-Donahou, Allison 24
 Dursahinhan, Altangerel **6**
 Dutton, Haley 14, 34, 37

E

Ebaugh, Dominick **122**
 Ekpo, Uwem 87
 Escobar-Alfonso, Santiago **11**, 14,
 34, 130
 Eshleman, Madison 94, 95, **116**
 Euclide, Elliana 103, **115**

F

Fabrizio, Makala 7, 36, 107
 Fauver, Joseph 58
 Fedders, Rachel 49
 Finch, Abigail **1**, 22, 98, **123**
 Fry, Lucy 44, 72

G

Gagne, Roderick 78
 Garcia, Julian **92**
 Gardner, Scott 6
 Gerrish, Gretchen 109
 Gilleard, John 89
 Gillis, Kathleen 79
 Goffinet, Bernard 84
 Goldy, Connor **10**
 Gonzalez, Tomas Acuña 36
 Goodman, Graham **66**

Gordillo-González, Daniel **14**, 34, 37, 130
Greggs, Jazmyn **74**
Greiman, Stephen 12, 13, 36, 76, 124
Groves, Jasmine **9**, 55, 76
Gudmundson, Amy 123
Gupta, Shruti 88, **91**

H

Haag, Eric 120
Hallett, Sascha 31
Hamik, Jeff 58
Hanelt, Ben 40, 63, **64**
Hanselman, Katherine **4**
Harris, Tyler 107
Harrison, Don 107
Hatlestad, Erik **40**
Hawdon, John 17, 20
Hechinger, Ryan 23, 26
Hernandez, Alexander 103, 115, 122
Hernandez-Trochez, Ash **112**
Herrmann, Kristin 36, **65**
Herzog, Kaylee **58**, **85**
Hilber, Alexia **50**
Hnida, John **38**
Hoffeditz, Elizabeth 103, 115
Holten, Zoe Von **12**, 36, 107
Hopkins, Skylar 2, 98
Horan, Sydney **29**, **131**
Hornung, Nathaniel 107, **129**
Horton, Matthew 130
Hotopp, Julie Dunning 120
Hughes, Lydia **99**

J

Jackson, Catherine **20**
Jacob, Solomon 87
Jensen, Kirsten 4, 36, **59**, 125
Jensen, Oliver **101**
Jergensen, Eric **105**
Jesus, Flavia Neto de 72
Jiménez, Agustín 63, **83**
Johnson, Oscar 112
Johnson, Pieter 55, 76
Jones, Alex 66
Jung, Suk Yul **121**

K

Kadam, Purvesh **90**
Kamasah, Japhet 52
Kang, Jesse 52
Kashyap, Sudhanva **88**, 90, 91, 92, 101
Keel, Matthew 128
Keeley, William 55

Keiser, Carl **111**
Kennedy, Molly **125**
Kerstetter, David 27, 48, 50, 93, 106
Kim, Eun-Jung 121
Kinsella, John 76
Kinsella, Mike 7, 107
Koch, Ryan **78**, 127
Koehne, Hutton 52
Kolman, Jon 77
Korpita, Timothy 51
Krause, Hayden **31**
Kroll, Mia 116
Kruth, Parryn 43
Kuris, Armand 23, 26

L

Lafferty, Kevin 23, 26
Lagrué, Clément 8
Landis, Cassidy 94, 95, 96
Langford, Gabriel 24, 47, 49, 126, 127
Langford, Melanie 24
Lantigua, Valerie 89
Lee, Alice **89**
Lekired, Abdelmalek **75**
Lewis, Noah **135**
Li, Virginia 10
Lighthall, Jake **118**
Lindo, Daniel 32
Lo, Eugenia 41
Locke, Sean 36
Long, Delaney **46**
Lowell, Andrew 20
Lu, Lijun **56**
Lukas, Biniyam 41

M

Makau-Barasa, Louise 87
Mamun, Tajul Islam **138**
Maness, Ryne **30**
Marcogliese, David 102
Markwith, Scott 119
Martinez, Eloy 27, 93
Martinez-Beltran, Stephanie **39**
Martínez-Rivera, Noraida 59
McCarthy, Cullen 10
McCormick, Dayna 58
McCowan, Connor **45**
McKean, Elise **17**
McKenzie, Valerie **51**
McKinstry, Cory 2
McLean, Bryan 12
McMahan, Sydnie 36, 59
Mekonen, Tibeb 120

Menard, Katrina 84
Mendez, Daphane 10
Metzger, Jake 67
Mevers, Emily 20
Miche, Sébastien 36
Mill, Nicholas 95
Minton, Brooklynn **24**
Mitreva, Makedonka 17
Montes, Martin 36
Moon, Miya **73**
Moore, Timothy 29
Moreno, Silvia 18

N

Nagel, Ema **106**
Neely, Wesley 2
Nelson, Alexandria **2**, **98**
Niedringhaus, Kevin 78
Niemann, Luke **113**
Nuss, Lily 58
Nycum, Taylor 89

O

O'Halloran, Damien 17
Odom, TJ 12
Ohran, Marissa **124**
Olariu, Alexander **69**
Olariu, Tudor 69
Olson, Sonja 53
Omoruyi, Zainab 87
Ortega, Felix Berrios **33**
Osanyinbi, Babatunde **87**
Oyarzun-Ruiz, Pablo 16

P

Pace, Eleanor 54
Page, Jim 7, 107, 136
Patch, Madison 66
Pella, Zach 58
Pena, Robert 10
Penalba, Fernanda Cortazar **134**
Pereira, Kenzie 2, 98
Peters, Nathan 72
Petter, Cory 94, 95, 116
Pfau, Russell 36
Phillips, Anna **86**
Pietri, Jose 58
Pobirohin, Valeria 22
Poholek, Ariel 137
Poslednik, Anna 55
Poulin, Robert 8
Pritchard, Jonathon 107, 128, 136

R

Rackliffe, Riley 10
Ramsingh, Brooke 128
Redman, Elizabeth 89
Reinfeld, Lauren **95**
Reyda, Florian 7, 46, 107
Richard, Alexandra 52
Rizzuti, Chiara **23**
Rodrigue, Juliette **28**
Rodriguez, David 2
Rosch, Cristen 122
Rothermel, Betsie 49
Rotolo, Jessica 32, **60**
Rowe, Matthew 136
Roys, Hayden 44, 72
Rycek, Eleni **132**

S

Saeij, Jeroen 39
Salvo, Andrew Di 78
Sangare, Lamba 19, 42
Santamaria, Carlos 79
Sargent, Sarah **48**
Schamberger, Gideon 94, **96**
Seminoff, Cassandra 94, 95
Serre, David 41
Shah, Naresh Kumar **68**
Sharma, Homa 52, 74
Shea, John 101, **108**
Sheehan, Kate **62**, 97, 104, 105
Shenkutie, Tassew 41
Shiina, Takuma 25
Shr, Victor 98
Silvennoinen, Jasmine **137**
Singer, Maiya 94, 95
Siqueira, Caroline de Moraes de 39

Smith, Christine 14, **34**
Smith, Halie 58
Smith, Mia 52
Smith, Nancy 99
Smith, Ryan 58
Stephan, Douglas **3**
Stover, Kevin 103
Stuart, Bailey 53
Stutler, Matthew **133**
Suelto, Jorrico 90, 92
Sundstrom, Kellee 58
Swanteson-Franz, Rachel 64
Sypher, Sasha **26**
Szelistowski, William 99

T

Tadjuidje, Emmanuel 52
Tesebay, Daniel 41
Thorn, Chelsea **70**
Thorning, Ethan 25
Tinsley, Malia 112
Tkach, Vasyl 7, 36, 76, 107, 128, 129, 136
Todd, Alexa **32**
Tolosa, Tirusew 41
Torres, Ariadna 25
Truong, Triet 14, 34
Tucker, Kimberly **94**, 95
Tucker, Matthew 94, 95, 96, 116
Turner, Thomas 25

U

Ulseth, Emma **114**

V

Valencia, Jesu 95

Venugopal, Gopinath 44
Vercellini, Clara 36
Vermeer, Sierrah 77
Voth, Daniel 44

W

Waddle, Kari 36
Walker, Liza 79
Warren, Micah 14, **15**, 34, 37
Washam, Charity 44
Weid, Pierre-Yves von der 72
Weinkopff, Tiffany **44**, **72**
Weinstein, Sara 66
Wenk, Laura 107, 136
Whale, Julia 32
Wheeler, Nicolas **53**
Williams, Netanya **5**
Willse, Blair **119**
Winningham, Kelly 130
Wragge, Jacob 88, 90, 91, 92

Y

Yamamoto, Masahiro 44
Yang, Seyoung 121
Yewhalaw, Delenesaw 41
Young, Maggie **7**, 76, **107**, 128, 129, 136

Z

Zaffiro, Briana **27**, **93**
Zhang, Si-Ming 75
Zhou-Hackbarth, Kevin **120**
Zimmermann, Michael **54**, **67**
Zincone, Matthew 20

Notes

ASP Meeting History

1925	Kansas City MO	1960	Los Angeles CA *	1995	Pittsburgh PA II
1926	Philadelphia PA	1961	Lafayette IN ‡	1996	Tucson AZ **
1927	Nashville TN	1962	Washington DC +	1997	Nashville TN
1928	New York NY	1963	Chicago IL *	1998	Kona HI
1929	Des Moines IA	1964	Boulder CO ‡	1999	Monterey CA ++
1930	Cleveland OH *	1965	Atlanta GA	2000	San Juan PR **
1931	New Orleans LA	1966	San Juan PR *	2001	Albuquerque NM
1932	Atlantic City NJ	1967	Tucson AZ §	2002	Vancouver BC Canada ¶ ss
1933	Boston MA	1968	Madison WI ‡	2003	Halifax NS Canada
1934	Pittsburgh PA	1969	Washington *	2004	Philadelphia PA II
1935	St Louis MO	1970	Washington DC ¶	2005	Mobile AL
1936	Atlantic City NJ	1971	Los Angeles CA	2006	Glasgow ¶
1937	Indianapolis IN	1972	Miami Beach FL *	2007	Merida Mexico ‡ ss
1938	Richmond VA	1973	Toronto ON Canada	2008	Arlington TX
1939	Columbus OH	1974	Kansas City MO	2009	Knoxville TN
1940	Philadelphia PA	1975	New Orleans LA *	2010	Colorado Springs CO
1941	Dallas TX	1976	San Antonio TX	2011	Anchorage AK
1942	No meeting	1977	Las Vegas NV	2012	Richmond VA
1943	No meeting	1978	Chicago IL *	2013	Quebec City QC Canada ¶¶
1944	Cleveland OH	1979	Minneapolis MN	2014	New Orleans LA
1945	St. Louis MO	1980	Berkeley CA	2015	Omaha NE
1946	Boston MA	1981	Montreal QB Canada	2016	Edmonton AB Canada
1947	Chicago IL	1982	Toronto ¶	2017	San Antonio TX ##
1948	New Orleans LA *	1983	San Antonio TX *	2018	Cancun Mexico
1949	New York NY	1984	Snowbird UT	2019	Rochester MN
1950	Cleveland OH	1985	Athens GA	2020	Cancelled
1951	Chicago IL *	1986	Denver CO *	2021	Virtual Online
1952	Ithaca NY ‡	1987	Lincoln NE #	2022	College Station TX
1953	Madison WI ‡	1988	Winston-Salem NC	2023	Kansas City MO
1954	Memphis TN *	1989	Vancouver BC Canada	2024	Denver CO
1955	Atlanta GA	1990	East Lansing MI	2025	Winston-Salem NC
1956	Storrs CT ‡	1991	Madison WI	2026	Orlando FL
1957	Philadelphia PA *	1992	Philadelphia PA	2027	Auburn AL
1958	Bloomington IN ‡	1993	Atlanta GA *		
1959	University Park PA ‡	1994	Ft. Collins CO		

* With the American Society of Tropical Medicine; since 1952, American Society of Tropical Medicine and Hygiene

+ With the Helminthological Society of Washington

‡ With the American Institute of Biological Sciences

§ With the American Microscopical Society

¶ With the International Congress of Parasitology; 1970 (ICOPA-II), 1982 (ICOPA-V), 2002 (ICOPA-X), 2006 (ICOPA-XI)

With the Wildlife Disease Association

II With the American Association of Veterinary Parasitologists

** With the Society of Protozoologists

++ With the Society of Nematologists

‡‡ With the Parasitology Section of the Canadian Society of Zoologists

ss With the Sociedad Mexicana de Parasitología

¶¶ With the Quebec Molecular Parasitology meeting

With the International Coccidiosis Conference